GenCore version 5.1.6
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Algorithm: pairwise scores, Gapped SW Model

Run on: December 5, 2002, 09:08:47 ; Search time 11.2 Seconds
(without alignments)
712.436 Million cell updates/sec

Title: US-09-503-387-3
Perfect score: 439
Sequence: 1 MSPSPIALPGLPMLSRVFA.....KSEEEIEIPL VVPPPLPL 439

Scoring table: GAPLIST
Gapop 10.0 , Gapext 10.0

Searched: 2047473 seqs, 2042202022 residues

Word size: 4

Total number of hits satisfying chosen parameters: 4094946

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database: Issued Patents AA:*
1: /cgn2_6/ptodata/1/iia/1A_PUBCOMB.pep:*
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5: /cgn2_6/ptodata/1/iia/3A_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/iia/3B_PUBCOMB.pep:*

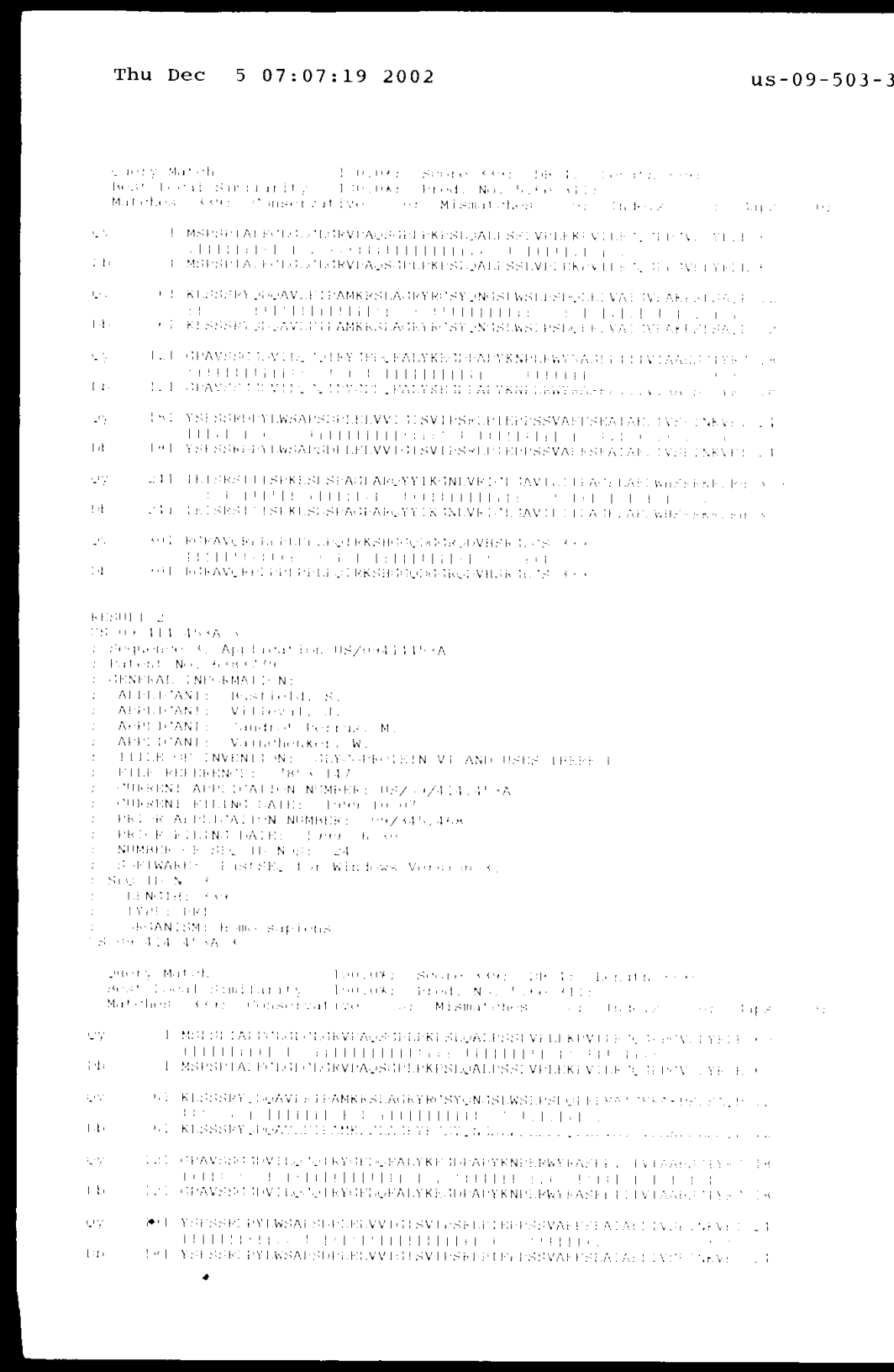
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	439	100.0	439	4	US-09-503-387-3	Sequence 3, Appli
2	439	100.0	439	3	US-09-414-459A-3	Sequence 3, Appli
3	439	94.1	439	4	US-09-503-468-5	Sequence 5, Appli
4	439	94.1	439	4	US-09-414-459A-5	Sequence 5, Appli
5	249	56.7	249	4	US-09-503-468-4	Sequence 4, Appli
6	249	56.7	249	4	US-09-414-459A-4	Sequence 4, Appli
7	61	13.9	51	4	US-09-503-468-1	Sequence 1, Appli
8	61	13.9	51	4	US-09-414-459A-1	Sequence 1, Appli
9	47	10.7	47	4	US-09-503-468-2	Sequence 2, Appli
10	47	10.7	47	4	US-09-414-459A-2	Sequence 2, Appli
11	41	12.1	41	4	US-09-503-468-6	Sequence 6, Appli
12	41	12.1	41	4	US-09-414-459A-6	Sequence 6, Appli
13	23	6.2	292	4	US-09-503-468-10	Sequence 10, Appl
14	23	6.2	292	4	US-09-414-459A-10	Sequence 10, Appl
15	23	6.2	292	4	US-09-503-468-18	Sequence 18, Appl
16	23	6.2	292	4	US-09-414-459A-18	Sequence 18, Appl
17	23	6.2	313	4	US-09-503-468-19	Sequence 19, Appl
18	23	6.2	313	4	US-09-414-459A-19	Sequence 19, Appl
19	2	5.9	20	4	US-09-503-468-3	Sequence 3, Appli
20	2	5.9	20	4	US-09-414-459A-3	Sequence 3, Appli
21	19	4.3	19	4	US-09-503-468-8	Sequence 8, Appli
22	19	4.3	19	4	US-09-414-459A-8	Sequence 8, Appli
23	19	4.3	47	4	US-09-503-468-23	Sequence 23, Appl
24	19	4.3	47	4	US-09-414-459A-23	Sequence 23, Appl
25	11	3.2	253	4	US-09-503-468-11	Sequence 11, Appl
26	11	3.2	255	4	US-09-503-468-31	Sequence 31, Appl
27	11	3.2	287	4	US-09-503-468-32	Sequence 32, Appl
28	11	3.2	289	4	US-09-503-468-12	Sequence 12, Appl
29	11	3.2	289	4	US-08-842-248A-12	Sequence 12, Appl
30	11	3.2	294	4	US-09-503-468-5	Sequence 5, Appli
31	11	3.2	306	4	US-09-503-468-14	Sequence 14, Appl
32	11	3.2	309	4	US-08-842-248A-14	Sequence 14, Appl
33	10	2.9	314	4	US-08-985-950-12	Sequence 12, Appl
34	10	2.9	314	4	US-09-503-468-8	Sequence 8, Appli
35	10	2.9	317	4	US-08-842-248A-8	Sequence 8, Appli
36	10	2.9	339	3	US-09-503-468-16	Sequence 16, Appl
37	10	2.9	339	3	US-08-842-248A-9	Sequence 16, Appl
38	10	2.9	414	4	US-09-503-468-2	Sequence 2, Appli
39	10	2.9	414	4	US-08-842-248A-2	Sequence 2, Appli
40	10	2.9	431	4	US-08-985-950-22	Sequence 22, Appl
41	10	2.9	432	4	US-09-503-468-4	Sequence 4, Appli
42	10	2.9	432	4	US-08-842-248A-4	Sequence 4, Appli
43	9	2.7	31	4	US-09-503-468-22	Sequence 22, Appl
44	9	2.7	31	4	US-09-414-459A-22	Sequence 22, Appl
45	9	2.7	50	4	US-09-503-468-13	Sequence 13, Appl
46	9	2.7	50	4	US-09-414-459A-13	Sequence 13, Appl
47	9	2.7	171	4	US-08-818-112-113	Sequence 113, App
48	9	2.7	171	4	US-08-818-111-113	Sequence 113, App
49	9	2.7	171	4	US-09-066-956-113	Sequence 113, App
50	9	2.7	171	4	US-09-072-596-113	Sequence 113, App
51	8	2.4	11	1	PCT-US98-23344-21	Sequence 21, Appl
52	8	2.4	22	4	US-08-662-877-34	Sequence 34, Appl
53	8	2.4	22	4	US-08-476-515A-34	Sequence 34, Appl
54	8	2.4	25	4	US-08-662-999A-35	Sequence 35, Appl
55	8	2.4	25	4	US-09-066-128-35	Sequence 35, Appl
56	8	2.4	29	4	US-08-662-999A-23	Sequence 23, Appl
57	8	2.4	29	4	US-09-503-124-253	Sequence 253, App
58	8	2.4	29	4	US-09-345-468-21	Sequence 21, Appl
59	8	2.4	31	4	US-09-414-459A-21	Sequence 21, Appl
60	8	2.4	31	4	US-09-345-468-21	Sequence 21, Appl
61	8	2.4	31	4	US-09-414-459A-21	Sequence 21, Appl
62	8	2.4	278	4	US-09-072-596-297	Sequence 297, App
63	8	2.4	311	3	US-08-985-950-14	Sequence 14, Appl
64	8	2.4	312	4	US-08-985-950-20	Sequence 20, Appl
65	8	2.4	316	4	US-09-503-468-18	Sequence 18, Appl
66	8	2.4	318	4	US-08-842-248A-18	Sequence 18, Appl
67	8	2.4	319	4	US-09-503-468-38	Sequence 38, Appl
68	8	2.4	319	4	US-09-410-466-22	Sequence 22, Appl
69	8	2.4	320	4	US-08-842-248A-22	Sequence 22, Appl
70	8	2.4	328	4	US-09-503-468-17	Sequence 17, Appl
71	8	2.4	328	4	US-08-842-248A-16	Sequence 17, Appl
72	8	2.4	329	4	US-08-985-950-16	Sequence 16, Appl
73	8	2.4	329	4	US-08-985-950-18	Sequence 18, Appl
74	8	2.4	331	4	US-09-345-468-12	Sequence 12, Appl
75	8	2.4	331	4	US-09-414-459A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-503-387-3
; Sequence 3, Application US/09503387
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeval, J.
; APPLICANT: Jandrot Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 785-127
; CURRENT APPLICATION NUMBER: US/09/503,387
; CURRENT FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-503-468-3



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; SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO 5
; LENGTH: [illegible]
; TYPE: [illegible]
; ORGANISM: Homo sapiens
US-09-414-45A-5

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Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

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Qy [illegible]
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Db [illegible]

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RESULT 6
US-09-414-45A-6
; Sequence 6, Application US/09/414,45A
; Patent No. 6985779
; GENERAL INFORMATION:
; APPLICANT: Bostwick, S.
; APPLICANT: Villeval, L.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Valentenkov, N.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7859.147
; CURRENT APPLICATION NUMBER: US/09/414,45A
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-45A-6

Query Match [illegible]; Score [illegible]; DB 4; Length [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

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Db [illegible]

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Db [illegible]

Qy [illegible]
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Db [illegible]

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Db [illegible]

RESULT 7
US-09-503-387-3
; Sequence 3, Application US/09/503,387
; Patent No. 6485927
; GENERAL INFORMATION:
; APPLICANT: Bodnar, R.
; APPLICANT: Xu, W.
; APPLICANT: Hynes, R.
; TITLE OF INVENTION: Integrin Modulating Compounds and Methods of Use Thereof
; FILE REFERENCE: 10039-0020P1
; CURRENT APPLICATION NUMBER: US/09/503,387
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/120,168
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-503-387-3

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Best Local Similarity [illegible]; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

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Db [illegible]

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Db [illegible]

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RESULT 8
US-09-414-45A-8
; Sequence 8, Application US/09/414,45A
; Patent No. 6985779
; GENERAL INFORMATION:
; APPLICANT: Bodnar, R.
; APPLICANT: Villeval, L.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Valentenkov, N.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7859.147
; CURRENT APPLICATION NUMBER: US/09/414,45A
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-45A-8

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Best Local Similarity [illegible]; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

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Db [illegible]

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Db [illegible]

Qy [illegible]
Db [illegible]

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Db [illegible]

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Db [illegible]

Qy [illegible]
Db [illegible]

RESULT 9
US-09-414-45A-9
; Sequence 9, Application US/09/414,45A
; Patent No. 6985779
; GENERAL INFORMATION:
; APPLICANT: Bodnar, R.
; APPLICANT: Villeval, L.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Valentenkov, N.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7859.147
; CURRENT APPLICATION NUMBER: US/09/414,45A
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-45A-9

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Best Local Similarity [illegible]; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

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Db [illegible]

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Qy [illegible]
Db [illegible]

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Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

RESULT 10
US-09-503-387-10
; Sequence 10, Application US/09/503,387
; Patent No. 6485927
; GENERAL INFORMATION:
; APPLICANT: Bodnar, R.
; APPLICANT: Villeval, L.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Valentenkov, N.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7859.147
; CURRENT APPLICATION NUMBER: US/09/503,387
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 20
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-453A-20

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Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCTTAAGGGAACTTCCTTA 21
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Db 1 GGCCTTAAGGGAACTTCCTTA 21

RESULT 8
US-09-414-453A-2
; Sequence 2, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Bostick, S.
; APPLICANT: Villegas, J.
; APPLICANT: Jaudon-Bottino, M.
; APPLICANT: Vallecchiesser, W.
; TITLE OF INVENTION: SLAY-SER-GLN-IN VI AND USES THEREOF
; FILE REFERENCE: 7454.147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/434,468
; PRIOR FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-453A-2

Query Match 19.4%; Score 21; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCTTAAGGGAACTTCCTTA 21
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Db 32 GGCCTTAAGGGAACTTCCTTA 52

RESULT 9
US-09-414-453A-3
; Sequence 3, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Bostick, S.
; APPLICANT: Villegas, J.
; APPLICANT: Jaudon-Bottino, M.
; APPLICANT: Vallecchiesser, W.
; TITLE OF INVENTION: SLAY-SER-GLN-IN VI AND USES THEREOF
; FILE REFERENCE: 7454.147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/434,468
; PRIOR FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-453A-3

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Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCTTAAGGGAACTTCCTTA 21
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Db 32 GGCCTTAAGGGAACTTCCTTA 52

RESULT 10
US-09-415-468-2
; Sequence 2, Application US/09415468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Bostick, S.
; APPLICANT: Villegas, J.
; APPLICANT: Jaudon-Bottino, M.
; APPLICANT: Vallecchiesser, W.
; TITLE OF INVENTION: SLAY-SER-GLN-IN VI AND USES THEREOF
; FILE REFERENCE: 7454.147
; CURRENT APPLICATION NUMBER: US/09/415,468
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-415-468-2

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Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCTTAAGGGAACTTCCTTA 21
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Db 27 GGCCTTAAGGGAACTTCCTTA 47

RESULT 11
US-09-415-468-7
; Sequence 7, Application US/09415468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Bostick, S.
; APPLICANT: Villegas, J.
; APPLICANT: Jaudon-Bottino, M.
; APPLICANT: Vallecchiesser, W.
; TITLE OF INVENTION: SLAY-SER-GLN-IN VI AND USES THEREOF
; FILE REFERENCE: 7454.147
; CURRENT APPLICATION NUMBER: US/09/415,468
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-415-468-7

Query Match 19.4%; Score 21; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCTTAAGGGAACTTCCTTA 21
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Db 21 GGCCTTAAGGGAACTTCCTTA 41

RESULT 12
US-09-414-453A-6
; Sequence 6, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Bostick, S.

```
; APPLICANT: Villeval, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7854.147
; CURRENT APPLICATION NUMBER: US/09/411,454A
; CURRENT FILING DATE: 1999-10-02
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 42
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-411-454A-9

  Query Match          12.2%;  Score 41;  DB 4;  Length 42;
  Best Local Similarity   78.0%;  Pred. No. 1.2e+03;
  Matches   32;  Conservative    0;  Mismatches    9;  Indels    2;  Gaps    1;

Qy      10 CCAGTTGTGTTTCTTGTCTCAGGTTCCAGTTTTTAAAGGAAAGCAAGTCTTCC 63
           ||||| |||||||||||| | |||| |||||||||| |
Db       1 CCAGTTGTGTTTCTTGTCTCAGGTTCCAGTTTTTAAAGGAAAGCAAGTCTTCC 54


RESULT 10
US-09-345-468-10
; Sequence 10, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
;  APPLICANT: Bodsted, S.
;  APPLICANT: Villeval, J.
;  APPLICANT: Jandrot-Perrus, M.
;  APPLICANT: Vainchenker, W.
;  TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
;  FILE REFERENCE: 7854.147
;  CURRENT APPLICATION NUMBER: US/09/345,468
;  CURRENT FILING DATE: 1999-06-30
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 267
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-345-468-10

  Query Match          12.2%;  Score 41;  DB 4;  Length 267;
  Best Local Similarity   78.0%;  Pred. No. 1.2e+03;
  Matches   32;  Conservative    0;  Mismatches    9;  Indels    2;  Gaps    1;

Qy      10 CCAGTTGTGTTTCTTGTCTCAGGTTCCAGTTTTTAAAGGAAAGCAAGTCTTCC 63
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Db      10 CCAGTTGTGTTTCTTGTCTCAGGTTCCAGTTTTTAAAGGAAAGCAAGTCTTCC 63


RESULT 15
US-09-345-468-15
; Sequence 15, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
;  APPLICANT: Bodsted, S.
;  APPLICANT: Villeval, J.
;  APPLICANT: Jandrot-Perrus, M.
;  APPLICANT: Vainchenker, W.
;  TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
;  FILE REFERENCE: 7854.147
;  CURRENT APPLICATION NUMBER: US/09/345,468
;  CURRENT FILING DATE: 1999-06-30
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-345-468-15

  Query Match          12.2%;  Score 41;  DB 4;  Length 294;
  Best Local Similarity   78.0%;  Pred. No. 1.2e+03;
  Matches   32;  Conservative    0;  Mismatches    9;  Indels    2;  Gaps    1;

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Db      10 CCAGTTGTGTTTCTTGTCTCAGGTTCCAGTTTTTAAAGGAAAGCAAGTCTTCC 63


RESULT 16
US-09-414-454A-16
; Sequence 16, Application US/09414454A
; Patent No. 6083729
; GENERAL INFORMATION:
;  APPLICANT: Bodsted, S.
;  APPLICANT: Villeval, J.
;  APPLICANT: Jandrot-Perrus, M.
;  APPLICANT: Vainchenker, W.
;  TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
;  FILE REFERENCE: 7854.147
;  CURRENT APPLICATION NUMBER: US/09/411,454A
;  CURRENT FILING DATE: 1999-10-02
;  PRIOR APPLICATION NUMBER: 09/345,468
;  PRIOR FILING DATE: 1999-06-30
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-414-454A-16

  Query Match          12.2%;  Score 41;  DB 4;  Length 294;
  Best Local Similarity   78.0%;  Pred. No. 1.2e+03;
  Matches   32;  Conservative    0;  Mismatches    9;  Indels    2;  Gaps    1;

Qy      10 CCAGTTGTGTTTCTTGTCTCAGGTTCCAGTTTTTAAAGGAAAGCAAGTCTTCC 63
           ||||| |||||||||||| | |||| |||||||||| |
Db      10 CCAGTTGTGTTTCTTGTCTCAGGTTCCAGTTTTTAAAGGAAAGCAAGTCTTCC 63
```

RESULT 17
US-09-445-408-16
; Sequence 16, Application US/09445408
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Bostwick, S.
; APPLICANT: Villocal, J.
; APPLICANT: Jandrot Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7854.147
; CURRENT APPLICATION NUMBER: US/09/445,408
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-445-408-16

Query Match 5.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSESPALEPLGLGLGPVFA 20
|||||||||||||||||||| |
Db 1 MSESPALEPLGLGLGPVFA 20

RESULT 18
US-09-414-45A-16
; Sequence 16, Application US/09414454A
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Bostwick, S.
; APPLICANT: Villocal, J.
; APPLICANT: Jandrot Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7854.147
; CURRENT APPLICATION NUMBER: US/09/414,454A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/445,408
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-45A-16

Query Match 5.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSESPALEPLGLGLGPVFA 20
|||||||||||||||||||| |
Db 1 MSESPALEPLGLGLGPVFA 20

RESULT 19
US-09-445-408-8
; Sequence 8, Application US/09445408
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Bostwick, S.
; APPLICANT: Villocal, J.
; APPLICANT: Jandrot Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7854.147
; CURRENT APPLICATION NUMBER: US/09/445,408
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-445-408-8

Query Match 5.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSESPALEPLGLGLGPVFA 20
|||||||||||||||||||| |
Db 1 MSESPALEPLGLGLGPVFA 20

RESULT 20
US-09-414-45A-8
; Sequence 8, Application US/09414454A
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Bostwick, S.
; APPLICANT: Villocal, J.
; APPLICANT: Jandrot Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7854.147
; CURRENT APPLICATION NUMBER: US/09/414,454A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/445,408
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-45A-8

Query Match 5.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSESPALEPLGLGLGPVFA 20
|||||||||||||||||||| |
Db 1 MSESPALEPLGLGLGPVFA 20

RESULT 21
US-09-445-408-8
; Sequence 8, Application US/09445408
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Bostwick, S.
; APPLICANT: Villocal, J.
; APPLICANT: Jandrot Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7854.147
; CURRENT APPLICATION NUMBER: US/09/445,408
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT

; ORGANISM: Bos taurus
US-09-503-387-3

Query Match 5.6%; Score 14; DB 1; Length 23
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 CVPCTGAVECCIACPLA 30
|||||||||||||||
Db 1 CVPCTGAVECCIACPLA 15

RESULT 22
US-09-414-455A-8
; Sequence 8, Application US/09414455A
; Patent No. 6468737
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeval, J.
; APPLICANT: Gachet Torres, M.
; APPLICANT: Valtchenkov, V.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THERE
; FILE REFERENCE: 7855.147
; CURRENT APPLICATION NUMBER: US/09/414,455A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-414-455A-8

Query Match 5.6%; Score 14; DB 1; Length 19
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 270 CVPCTGAVECCIACPLA 283
|||||||||||||||
Db 4 CVPCTGAVECCIACPLA 19

RESULT 23
US-09-345-459-23
; Sequence 23, Application US/09345459
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeval, J.
; APPLICANT: Gachet Torres, M.
; APPLICANT: Valtchenkov, V.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THERE
; FILE REFERENCE: 7855.147
; CURRENT APPLICATION NUMBER: US/09/345,459
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-345-459-23

Query Match 4.7%; Score 12; DB 1; Length 47
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 EPCIVIAABSGIYGC 179
||||||||||||||
Db 32 EPCIVIAABSGIYGC 47

RESULT 24
US-09-414-455A-23
; Sequence 23, Application US/09414455A
; Patent No. 6468737
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeval, J.
; APPLICANT: Gachet Torres, M.
; APPLICANT: Valtchenkov, V.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THERE
; FILE REFERENCE: 7855.147
; CURRENT APPLICATION NUMBER: US/09/414,455A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-414-455A-23

Query Match 4.7%; Score 12; DB 1; Length 47
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 EPCIVIAABSGIYGC 179
||||||||||||||
Db 32 EPCIVIAABSGIYGC 47

RESULT 25
US-09-345-459-36
; Sequence 36, Application US/09345459
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Borges, Luis
; TITLE OF INVENTION: Family of Immunoregulatory Designated to Encode Immune
; TITLE OF INVENTION: Cell Receptors (CIR)
; FILE REFERENCE: 2524.A
; CURRENT APPLICATION NUMBER: US/09/345,459.A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 60/112,240
; EARLIER FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-09-345-459-36

Query Match 4.2%; Score 11; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 PSDELELVVEG 204
|||||||||||
Db 117 PSDELELVVEG 127

RESULT 26
US-09-345-459-34
; Sequence 34, Application US/09345459A
; Patent No. 6468203
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Borges, Luis

; TITLE OF INVENTION: Family of Immunostimulatory Oligonucleotides
; TITLE OF INVENTION: Like Receptors (LTR)
; FILE REFERENCE: 2621.A
; CURRENT APPLICATION NUMBER: US/09/503,387A
; CURRENT FILING DATE: 2000-02-12
; EARLIER APPLICATION NUMBER: 08/842,240
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Human
US-09-503-387-41

Query Match 4.2%; Score 11; DB 4; Length 24
Best Local Similarity 100.0%; Pred. No. 1.1e+03
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 TGTCGTTGTCGT 12
|||||||||||| |
Db 1 TGTCGTTGTCGT 12

RESULT 27
US-09-503-387-2
; Sequence 2, Application US/09503387A
; Patent No. 6444806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Bergan, Lois
; TITLE OF INVENTION: Family of Immunostimulatory Oligonucleotides
; TITLE OF INVENTION: Like Receptors (LTR)
; FILE REFERENCE: 2621.A
; CURRENT APPLICATION NUMBER: US/09/503,387A
; CURRENT FILING DATE: 2000-02-12
; EARLIER APPLICATION NUMBER: 08/842,240
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 287
; TYPE: DNA
; ORGANISM: Human
US-09-503-387-2

Query Match 4.2%; Score 11; DB 4; Length 287
Best Local Similarity 100.0%; Pred. No. 1.1e+04
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 TGTCGTTGTCGT 12
|||||||||||| |
Db 1 TGTCGTTGTCGT 12

RESULT 28
US-09-503-387-1
; Sequence 1, Application US/09503387A
; Patent No. 6444806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Bergan, Lois
; TITLE OF INVENTION: Family of Immunostimulatory Oligonucleotides
; TITLE OF INVENTION: Like Receptors (LTR)
; FILE REFERENCE: 2621.A
; CURRENT APPLICATION NUMBER: US/09/503,387A
; CURRENT FILING DATE: 2000-02-12
; EARLIER APPLICATION NUMBER: 08/842,240
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 269
; TYPE: DNA
; ORGANISM: Human
US-09-503-387-1

Query Match 4.2%; Score 11; DB 4; Length 269
Best Local Similarity 100.0%; Pred. No. 1.1e+03
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 TGTCGTTGTCGT 12
|||||||||||| |
Db 1 TGTCGTTGTCGT 12

RESULT 29
US-08-842,240A-12
; Sequence 12, Application US/08842240A
; Patent No. 6444806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Anderson, David E.
; TITLE OF INVENTION: Family of Immunostimulatory Oligonucleotides
; TITLE OF INVENTION: Like Receptors (LTR)
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon, Henry, Intellectual Property Group
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,240A
; FILING DATE: April 24, 1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Carlos A.
; REGISTRATION NUMBER: 34,447
; REFERENCE/DOCKET NUMBER: 2621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 759822
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-842,240A-12

Query Match 4.2%; Score 11; DB 4; Length 269
Best Local Similarity 100.0%; Pred. No. 1.1e+03
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 TGTCGTTGTCGT 12
|||||||||||| |
Db 1 TGTCGTTGTCGT 12

RESULT 30
US-09-503-387-30
; Sequence 30, Application US/09503387A
; Patent No. 6444806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Bergan, Lois

; TITLE OF INVENTION: Family of Immunostimulatory Polynucleotides and Methods of Using Same
; TITLE OF INVENTION: Like Receptors (TLR)
; FILE REFERENCE: 2624.A
; CURRENT APPLICATION NUMBER: US/09/503,387-A
; CURRENT FILING DATE: 2000-02-12
; PRIOR APPLICATION NUMBER: 60/042,240
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-503-387-3

Query Match 5.2%; Score 11; DB 11; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 11; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 194 GSGGELVVIG 204
|||||||||||
Db 127 GSGGELVVIG 137

RESULT 4
US-09-503-387-14
; Sequence 14, Application US/09503387A
; Patent No. 6642207
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Borges, Luis
; TITLE OF INVENTION: Family of Immunostimulatory Polynucleotides and Methods of Using Same
; TITLE OF INVENTION: Like Receptors (TLR)
; FILE REFERENCE: 2624.A
; CURRENT APPLICATION NUMBER: US/09/503,387-A
; CURRENT FILING DATE: 2000-02-12
; PRIOR APPLICATION NUMBER: 60/042,240
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Human
US-09-503-387-14

Query Match 5.2%; Score 11; DB 11; Length 460;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 194 GSGGELVVIG 204
|||||||||||
Db 354 GSGGELVVIG 364

RESULT 5
US-09-503-387-4
; Sequence 4, Application US/08812249A
; Patent No. 6130085
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Family of Immunostimulatory Polynucleotides and Methods of Using Same
; TITLE OF INVENTION: Like Receptors (TLR)
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lynn C. Henry, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,249A
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,279
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,383
; FILING DATE: 15-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,252
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Edward F.
; REGISTRATION NUMBER: 34,526
; REFERENCE/DOCKET NUMBER: 2624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-503-387-4

Query Match 5.2%; Score 11; DB 4; Length 489;
Best Local Similarity 50.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 194 GSGGELVVIG 204
|||||||||||
Db 127 GSGGELVVIG 137

RESULT 6
US-09-503-387-12
; Sequence 12, Application US/09503387A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte-Derived Dendritic
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Ave
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,387
; FILING DATE: 05-FEB-2000
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/034,279
; FILING DATE: 21-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/812,249
; FILING DATE: 05-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,383
; FILING DATE: 15-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,252
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Edward F.
; REGISTRATION NUMBER: 34,526
; REFERENCE/DOCKET NUMBER: DNX-20K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)812-1770
; TELEFAX: (650)496-1200

Query Match 5.2%; Score 11; DB 4; Length 1***;
Best Local Similarity 50.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 194 GSGGELVVIG 204
|||||||||||
Db 179 GSGGELVVIG 189

RESULT 13
US-09-503-387-12
; Sequence 12, Application US/09503387A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte-Derived Dendritic
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Ave
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,387
; FILING DATE: 05-FEB-2000
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/034,279
; FILING DATE: 21-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/812,249
; FILING DATE: 05-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,383
; FILING DATE: 15-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,252
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Edward F.
; REGISTRATION NUMBER: 34,526
; REFERENCE/DOCKET NUMBER: DNX-20K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)812-1770
; TELEFAX: (650)496-1200

```
;    INFORMATION FOR SEQ ID NO:  12
;      SEQUENCE CHARACTERISTICS:
;        LENGTH:  439 amino acids
;        TYPE:  amino acid
;        STRANDEDNESS:  linear
;      MOLECULE TYPE:  protein
US-08-503-387-3-12

  Query Match                 27.9%;  Score 102;  DB 4;  Length 439;
  Best Local Similarity   30.0%;  Pred. No. 2.1e-11;
  Matches  34;  Conservative  31;  Mismatches  71;  Indels  14;  Gaps  4;

Qy      195 SSPSELVVTG 204
            S P  L VTG
Db      211 SLPGLVVTG 220


RESULT 13
US-09-503-387-3-8
; Sequence 8, Application US/09503387A
; Patent No. 6541209
; GENERAL INFORMATION:
;  APPLICANT: Osborn, David J.
;  APPLICANT: Anderson, Erik M.
;  APPLICANT: Borges, Luis
;  TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin
;  TITLE OF INVENTION: Like Receptors (LIR)
;  FILE REFERENCE: 2424.A
;  CURRENT APPLICATION NUMBER: US/09/503,387A
;  CURRENT FILING DATE: 1999-02-12
;  PRIOR APPLICATION NUMBER: 08/842,240
;  PRIOR FILING DATE: 1997-04-24
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;    LENGTH: 439
;    TYPE: PRT
;    ORGANISM: Human
US-09-503-387-3-8

  Query Match                 27.9%;  Score 102;  DB 4;  Length 439;
  Best Local Similarity   30.0%;  Pred. No. 2.1e-11;
  Matches  34;  Conservative  31;  Mismatches  71;  Indels  14;  Gaps  4;

Qy      195 SSPSELVVTG 204
            S P  L VTG
Db      211 SLPGLVVTG 220


RESULT 14
US-08-842-240A-8
; Sequence 8, Application US/08842240A
; Patent No. 6448385
;  GENERAL INFORMATION:
;    APPLICANT:  Osborn, David J.
;    TITLE OF INVENTION:  Family of Immunoregulators
;    TITLE OF INVENTION:  Leukocyte Immunoglobulin-like Receptors (LIR)
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janis C. Berry, Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  US
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk
;      COMPUTER:  IBM/PC Compatible
;      OPERATING SYSTEM:  Microsoft Word 7
;      SOFTWARE:  PatentIn Release #1.0, Version #1.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/842,240A
;      FILING DATE:  April 24, 1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berry, Janis C.
;      REGISTRATION NUMBER:  34,467
;      REFERENCE/DOCKET NUMBER:  2424
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  439 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-842-240A-8

  Query Match                 27.9%;  Score 102;  DB 4;  Length 439;
  Best Local Similarity   30.0%;  Pred. No. 2.1e-11;
  Matches  34;  Conservative  31;  Mismatches  71;  Indels  14;  Gaps  4;

Qy      195 SSPSELVVTG 204
            S P  L VTG
Db      211 SLPGLVVTG 220


RESULT 15
US-08-842-240A-10
; Sequence 10, Application US/08842240A
; Patent No. 6448385
; GENERAL INFORMATION:
;  APPLICANT: Osborn, David J.
;  APPLICANT: Anderson, Erik M.
;  APPLICANT: Borges, Luis
;  TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin
;  TITLE OF INVENTION: Like Receptors (LIR)
;  FILE REFERENCE: 2424.A
;  CURRENT APPLICATION NUMBER: US/09/503,387A
;  CURRENT FILING DATE: 1999-02-12
;  PRIOR APPLICATION NUMBER: 08/842,240
;  PRIOR FILING DATE: 1997-04-24
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;    LENGTH: 439
;    TYPE: PRT
;    ORGANISM: Human
US-09-503-387-3-10

  Query Match                 27.9%;  Score 102;  DB 4;  Length 439;
  Best Local Similarity   30.0%;  Pred. No. 2.1e-11;
  Matches  34;  Conservative  31;  Mismatches  71;  Indels  14;  Gaps  4;

Qy      195 SSPSELVVTG 204
            S P  L VTG
Db      211 SLPGLVVTG 220


RESULT 17
US-08-842-240A-10
; Sequence 10, Application US/08842240A
; Patent No. 6448385
;  GENERAL INFORMATION:
;    APPLICANT:  Osborn, David J.
;    TITLE OF INVENTION:  Family of Immunoregulators Designated
;    TITLE OF INVENTION:  Leukocyte Immunoglobulin-like Receptors (LIR)
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janis C. Berry, Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  US
```

; APPLICANT: Osborn, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Berges, Lois
; TITLE OF INVENTION: Family of [illegible] Like Receptors (LIR)
; FILE REFERENCE: 2624.A
; CURRENT APPLICATION NUMBER: US/09/[illegible]
; CURRENT FILING DATE: 1999-05-12
; EARLIEST APPLICATION NUMBER: US/08/[illegible]
; EARLIEST FILING DATE: [illegible]
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: [illegible]
; TYPE: PRT
; ORGANISM: Human
US-09-[illegible]-2

Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

Qy [illegible] SGSEIVVQS 254
[illegible]
Db [illegible] SGSEIVVQS 118

RESULT 58
US-09-[illegible]-2
; Sequence 2, Application US/[illegible]A
; Patent No. [illegible]
; GENERAL INFORMATION:
; APPLICANT: Osborn, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Berges, Lois
; TITLE OF INVENTION: Family of [illegible] Like Receptors (LIR)
; FILE REFERENCE: 2624.A
; CURRENT APPLICATION NUMBER: US/09/[illegible]A
; CURRENT FILING DATE: 1999-05-12
; EARLIEST APPLICATION NUMBER: US/08/[illegible]
; EARLIEST FILING DATE: [illegible]
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: [illegible]
; TYPE: PRT
; ORGANISM: Human
US-09-[illegible]-2

Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

Qy [illegible] SGSEIVVQS 254
[illegible]
Db [illegible] SGSEIVVQS 120

RESULT 59
US-09-[illegible]-2
; Sequence 2, Application US/[illegible]A
; Patent No. [illegible]
; GENERAL INFORMATION:
; APPLICANT: Osborn, David J.
; TITLE OF INVENTION: Family of [illegible] Like Receptors (LIR)
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/[illegible]
; FILING DATE: 05-JAN-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US [illegible]
; FILING DATE: 21-MAR-[illegible]
; PRIOR APPLICATION DATA
; APPLICATION NUMBER: US [illegible]

; FILING DATE: [illegible]
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/[illegible]
; FILING DATE: [illegible]
; ATTORNEY/AGENT INFORMATION:
; NAME: [illegible]
; REGISTRATION NUMBER: [illegible]
; REFERENCE/DOCKET NUMBER: [illegible]
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: [illegible]
; TELEFAX: [illegible]
; INFORMATION FOR SEQ ID NO: [illegible]
; SEQUENCE CHARACTERISTICS:
; LENGTH: [illegible] amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US [illegible]

Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible] SGEIEVVEQ 284
[illegible]
Db [illegible] SGEIEVVEQ 120

RESULT 32
US-09-503-387-3
; Sequence 3, Application US/09503387A
; Patent No. 6994959
; GENERAL INFORMATION:
; APPLICANT: Tomasz Lipniacki
; APPLICANT: Andrzej Gorski, Jerzy M.
; APPLICANT: Bodnar, Lech
; TITLE OF INVENTION: Family of Immunomodulatory [illegible]
; TITLE OF INVENTION: Like Receptors (LIR)
; FILE REFERENCE: 2451.A
; CURRENT APPLICATION NUMBER: US/09/503,387A
; CURRENT FILING DATE: 2000-02-12
; EARLIER APPLICATION NUMBER: 60/120,249
; EARLIER FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Homo
US-09-503-387-3

Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible] SGEIEVVEQ 284
[illegible]
Db [illegible] SGEIEVVEQ 120

RESULT 33
US-09-842-240A-4
; Sequence 4, Application US/09842240A
; Patent No. 6811776
; GENERAL INFORMATION:
; APPLICANT: Tsumura, Yasuhiko
; APPLICANT: Ishimaru, Yoshiki
; TITLE OF INVENTION: Family of Immunomodulatory [illegible]
; TITLE OF INVENTION: Leukocyte Immunoglobulin-Like Receptors
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sakai T. Henry, Intellectual Property
; STREET: 701 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM/PC Compatible
; OPERATING SYSTEM: Microsoft Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/842,240A
; FILING DATE: April 24, 2001
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C.
; REGISTRATION NUMBER: 31,547
; REFERENCE/DOCKET NUMBER: 2724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0615
; TELEFAX: (206) 233-0644
; TELEX: 756622
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-842-240A-4

Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible] SGEIEVVEQ 284
[illegible]
Db [illegible] SGEIEVVEQ 120

RESULT 34
US-09-456-459A-22
; Sequence 22, Application US/09456459A
; Patent No. 6248927
; GENERAL INFORMATION:
; APPLICANT: Bostford, S.
; APPLICANT: Villeval, J.
; APPLICANT: Samuel Bolton, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7858.147
; CURRENT APPLICATION NUMBER: US/09/456,459A
; CURRENT FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-456-459A-22

Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible] VGEVEEKL 54
[illegible]
Db [illegible] VGEVEEKL 59

RESULT 35
US-09-456-459A-22
; Sequence 22, Application US/[illegible]
; Patent No. 6083729
; GENERAL INFORMATION:
; APPLICANT: Bostford, S.

; APPLICANT: Villet, C.
; APPLICANT: Jacobs, Peter S., M.
; APPLICANT: Viljoen, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 2454.147
; CURRENT APPLICATION NUMBER: US/09/414,454A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/047,140
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-414-454A-22

Query Match 2.7%; Score 94; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 VGLYRLEKL 62
||||||||| |
Db 7 VGLYRLEKL 15

RESULT 19
US-09-439-166-15
; Sequence 15, Application US/09439166
; Patent No. 6215027
; GENERAL INFORMATION:
; APPLICANT: Bielefeld, S.
; APPLICANT: Villeval, J.
; APPLICANT: Jandrot Perrus, M.
; APPLICANT: Villeneuker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 2454.147
; CURRENT APPLICATION NUMBER: US/09/439,166
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-439-166-15

Query Match 2.7%; Score 94; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 VGLYRLEKL 62
||||||||| |
Db 11 VGLYRLEKL 22

RESULT 20
US-09-414-454A-15
; Sequence 15, Application US/09414454A
; Patent No. 6403763
; GENERAL INFORMATION:
; APPLICANT: Bieleveld, S.
; APPLICANT: Villeval, J.
; APPLICANT: Jandrot Perrus, M.
; APPLICANT: Villeneuker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 2454.147
; CURRENT APPLICATION NUMBER: US/09/414,454A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/047,140
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-454A-15

Query Match 2.7%; Score 94; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 VGLYRLEKL 62
||||||||| |
Db 11 VGLYRLEKL 22

RESULT 21
US-09-414-454A-22
; Sequence 22, Application US/09414454A
; Patent No. 6403763
; GENERAL INFORMATION:
; APPLICANT: Bieleveld, S.
; APPLICANT: Villeval, J.
; APPLICANT: Jandrot Perrus, M.
; APPLICANT: Villeneuker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 2454.147
; CURRENT APPLICATION NUMBER: US/09/414,454A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/047,140
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-414-454A-22

Query Match 2.7%; Score 94; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 VGLYRLEKL 62
||||||||| |
Db 7 VGLYRLEKL 15

RESULT 22
US-08-478-112-14
; Sequence 14, Application US/08478112
; Patent No. 6290959
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven T.
; APPLICANT: Skolsky, Yaser A.W.
; APPLICANT: Dillon, Lisa C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Teodor
; TITLE OF INVENTION: METHODS AND MEDIUMS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND/OR ASSAYS FOR TUBERCULOSIS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,112
; FILING DATE: 15-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark, David C.
; REGISTRATION NUMBER: 41,429
; REFERENCE/DOCKET NUMBER: 259121.411US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-478-112-14

Query Match 2.7%; Score 94; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.0;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 508 PLRLEKLPEL 517
||||||||| |
Db 68 PLRLEKLPEL 77

RESULT 23
US-08-478-112-13

```
; Sequence 144, Application US/09503387
; Patent No. 6559042
; GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   APPLICANT: Skolky, Yasir A.W.
;   APPLICANT: Dillon, Dustin C.
;   APPLICANT: Corixa Corporation
;   APPLICANT: Houghton, Raymond
;   APPLICANT: Vedvick, Thomas S.
;   APPLICANT: Twardzik, Daniel R.
;   TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF [illegible]
;   NUMBER OF SEQUENCES: 154
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SEED and BERRY LLP
;     STREET: 6300 Columbia Center, 701 Fifth Avenue
;     CITY: Seattle
;     STATE: Washington
;     COUNTRY: USA
;     ZIP: 98104-7092
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/503,387
;     FILING DATE: 13-MAR-2000
;     CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Mohr, Judith L.
;     REGISTRATION NUMBER: 36,233
;     REFERENCE/DOCKET NUMBER: 2001.2.11
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (206) 622-4900
;     TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 144:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 134 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-503-387-144

  Query Match                 2.7%;  Score 9;  DB 1;  Length 134;
  Best Local Similarity   21.4%;  Pred. No. 2.4;
  Matches    3;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy     108 EEPEEPEEP 116
           : : : : :
Db      98 EEPEEPEEP 106


RESULT 145
US-09-503-387-145
; Sequence 145, Application US/09503387
; Patent No. 6559042
; GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   APPLICANT: Skolky, Yasir A.W.
;   APPLICANT: Dillon, Dustin C.
;   TITLE OF INVENTION: COMPOUNDS AND METHODS FOR [illegible] AND [illegible]
;   NUMBER OF SEQUENCES: 241
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SEED and BERRY LLP
;     STREET: 6300 Columbia Center, 701 Fifth Avenue
;     CITY: Seattle
;     STATE: Washington
;     COUNTRY: USA
;     ZIP: 98104-7092
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/503,387
;     FILING DATE: 09-MAY-1998
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Mohr, Judith L.
;     REGISTRATION NUMBER: 36,233
;     REFERENCE/DOCKET NUMBER: 2001.2.11
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (206) 622-4900
;     TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 145:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 134 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-503-387-145

  Query Match                 2.7%;  Score 9;  DB 1;  Length 134;
  Best Local Similarity   21.4%;  Pred. No. 2.4;
  Matches    3;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy     108 EEPEEPEEP 116
           : : : : :
Db      98 EEPEEPEEP 106


RESULT 146
US-09-503-387-146
; Sequence 146, Application US/09503387
; Patent No. 6458366
; GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   APPLICANT: Skolky, Yasir A.W.
;   APPLICANT: Dillon, Dustin C.
;   APPLICANT: Corixa Corporation
;   APPLICANT: Houghton, Raymond
;   APPLICANT: Vedvick, Thomas S.
;   APPLICANT: Twardzik, Daniel R.
;   APPLICANT: Probst, Michael R.
;   APPLICANT: Hendrickson, Edward R.
;   TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS [illegible]
;   NUMBER OF SEQUENCES: 154
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SEED and BERRY LLP
;     STREET: 6300 Columbia Center, 701 Fifth Avenue
;     CITY: Seattle
;     STATE: Washington
;     COUNTRY: USA
;     ZIP: 98104-7092
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/503,387
;     FILING DATE: 09-MAY-1998
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Mohr, Judith L.
;     REGISTRATION NUMBER: 36,233
;     REFERENCE/DOCKET NUMBER: 2001.2.11
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (206) 622-4900
;     TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 146:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 134 amino acids
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MPsearch, protein search, GSIsw3.0.dat

Run on: December 5, 2002, 06:55:17 ; Search time 0 Seconds
(without alignments)
[illegible] Million cell updates/sec

Title: US-09-503-387-3
Perfect score: 449
Sequence: 1 MSPSFALFCLHLGVFA.....LKSRSSLTPG, 449 aa

Scoring table: GLIC1
Gapop 6.0 , Gapext 0.0

Searched: 99847 seqs, 15250620 residues

Word size: 3

Total number of hits satisfying chosen parameters: 199694

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_120402:*
1: /SIDS2/gcgdata/Geneseq/Geneseq_emb1/AA_new.pep:*
2: /SIDS2/gcgdata/Geneseq/Geneseq_emb2/AA_new.pep:*
3: /SIDS2/gcgdata/Geneseq/Geneseq_emb3/AA_new.pep:*
4: /SIDS2/gcgdata/Geneseq/Geneseq_emb4/AA_new.pep:*
5: /SIDS2/gcgdata/Geneseq/Geneseq_emb5/AA_new.pep:*
6: /SIDS2/gcgdata/Geneseq/Geneseq_emb6/AA_new.pep:*
7: /SIDS2/gcgdata/Geneseq/Geneseq_emb7/AA_new.pep:*
8: /SIDS2/gcgdata/Geneseq/Geneseq_emb8/AA_new.pep:*
9: /SIDS2/gcgdata/Geneseq/Geneseq_emb9/AA_new.pep:*
10: /SIDS2/gcgdata/Geneseq/Geneseq_emb10/AA_new.pep:*
11: /SIDS2/gcgdata/Geneseq/Geneseq_emb11/AA_new.pep:*
12: /SIDS2/gcgdata/Geneseq/Geneseq_emb12/AA_new.pep:*
13: /SIDS2/gcgdata/Geneseq/Geneseq_emb13/AA_new.pep:*
14: /SIDS2/gcgdata/Geneseq/Geneseq_emb14/AA_new.pep:*
15: /SIDS2/gcgdata/Geneseq/Geneseq_emb15/AA_new.pep:*
16: /SIDS2/gcgdata/Geneseq/Geneseq_emb16/AA_new.pep:*
17: /SIDS2/gcgdata/Geneseq/Geneseq_emb17/AA_new.pep:*
18: /SIDS2/gcgdata/Geneseq/Geneseq_emb18/AA_new.pep:*
19: /SIDS2/gcgdata/Geneseq/Geneseq_emb19/AA_new.pep:*
20: /SIDS2/gcgdata/Geneseq/Geneseq_emb20/AA_new.pep:*
21: /SIDS2/gcgdata/Geneseq/Geneseq_emb21/AA_new.pep:*
22: /SIDS2/gcgdata/Geneseq/Geneseq_emb22/AA_new.pep:*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed,
assuming that the data fits the Extreme Value distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	449	100.0	449	22	AAB61265	Human IAN7 2nd p
2	434	96.7	434	22	AAB61267	Human IAN7 2nd p
3	434	96.7	434	22	AAB61268	Human IAN7 2nd p
4	432	96.2	449	22	AAB61273	Human IAN7 2nd p
5	428	95.3	449	22	AAB61274	Human IAN7 2nd p
6	424	94.4	434	22	AAB61271	Human IAN7 2nd p
7	416	92.6	434	22	AAY72705	Human platelet s
8	408	90.9	449	22	AAB61275	Human IAN7 2nd p
9	408	90.9	449	22	AAB61276	Human IAN7 2nd p
10	406	90.4	449	22	AAB61277	Human IAN7 2nd p

ALIGNMENTS

RESULT 1
AAB61265
ID AAB61265 standard; protein; 449 AA.

XX
AC AAB61257;
XX
DT 04-APR-2001 (first entry)
XX
DE Human IANG-268 protein.
XX
KW Human; IANG-268; cardiac; vascular protective; cytostatic; anti-atherosclerotic;
KW thrombolytic; antithrombosis; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Homo sapiens.
XX
RN W0200108681-A1.
XX
RD 01-FEB-2001.
XX
RP 27-JUL-2000; 2000WO-US020152.
XX
PR 28-JUL-1999; 99US-0145468.
PR 06-DEC-1999; 99US-0454024.
PR 14-FEB-2000; 2000US-0503387.
XX
PA (MILL) MILLENNIUM PHARM INC.
XX
PI Bosio A SJ, Villeda J, Zaldivar Peiras M, Valtenbrecher W, Sica DS;
PI Qian MD, Klingbeil G;
XX
DR WPI; 2001-186877/19.
XX
PT New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for prevention, treating
PT and diagnosing hemorrhagic disorders, thrombotic disorders and
PT immunological disorders
XX
PS Disclosure; Fig 2; 22pp; English.
XX
CC The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called IANG-268. The GPVI polypeptides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent and treat
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
SQ Sequence 268 AA;

Query Match 100.0%; Score 1455; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 6.2e-149;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPSPIALPTGLLGRVPAQSCLEKESLALLSTLVELEKVLAQTGSDLPEEP 52
Db 1 MSPSPIALPTGLLGRVPAQSCLEKESLALLSTLVELEKVLAQTGSDLPEEP 52

Qy 53 KLSSSKPQQGAVIIAMRLMASRPFVQGRSTWGSDLLSGKTPGAQCTDIL 102
Db 53 KLSSSKPQQGAVIIAMRLMASRPFVQGRSTWGSDLLSGKTPGAQCTDIL 102

Qy 103 QPAVSSGNGVILGQLPYGPLGLAGSSGGAYKNEDWTPASETLTIVTAAGL 152
Db 103 QPAVSSGNGVILGQLPYGPLGLAGSSGGAYKNEDWTPASETLTIVTAAGL 152

Qy 153 PEVPEVQNLTGAEVYSYLRVASPSVSLLISQSSDQGKSFLSVGDSWVPQY 202
Db 153 PEVPEVQNLTGAEVYSYLRVASPSVSLLISQSSDQGKSFLSVGDSWVPQY 202

Qy 203 EPMFRGRVRLYMGVTEHGLQAFHSMDIVEGPVILSGLTLYSIVGIHAKH 252
Db 203 EPMFRGRVRLYMGVTEHGLQAFHSMDIVEGPVILSGLTLYSIVGIHAKH 252

Qy 253 EAMETYEKIGSA 264
Db 253 EAMETYEKIGSA 264

RESULT 2
AAB61257
ID AAB61257 standard; protein; 268 AA.
XX
AC AAB61257;
XX
DT 04-APR-2001 (first entry)
XX
DE Mature human IANG-268 protein.
XX
KW Human; IANG-268; cardiac; cerebroprotective; cytostatic; anti-atherosclerotic;
KW thrombolytic; antithrombosis; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Homo sapiens.
XX
RN W0200108681-A1.
XX
RD 01-FEB-2001.
XX
RP 27-JUL-2000; 2000WO-US020152.
XX
PR 28-JUL-1999; 99US-0145468.
PR 06-DEC-1999; 99US-0454024.
PR 14-FEB-2000; 2000US-0503387.
XX
PA (MILL) MILLENNIUM PHARM INC.
XX
PI Bosio A SJ, Villeda J, Zaldivar Peiras M, Valtenbrecher W, Sica DS;
PI Qian MD, Klingbeil G;
XX
DR WPI; 2001-186877/19.
XX
PT New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for prevention, treating
PT and diagnosing hemorrhagic disorders, thrombotic disorders and
PT immunological disorders
XX
PS Disclosure; Fig 2; 22pp; English.
XX
CC The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called IANG-268. The GPVI polypeptides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent and treat
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.

XX
SQ Sequence 419 AA;

Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

RESULT 3
AAB64141
ID AAB64141 standard; protein; 419 AA.
XX
AC AAB64141;
XX
DT 30-APR-2001 (first entry)
XX
DE Human platelet glycoprotein VI mature protein.
XX
KW Human; thrombolytic; cardiovascular; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein; platelet activation;
KW platelet collagen interaction; thrombotic disorder;
KW cardiovascular disorder.
XX
OS Homo sapiens.
XX
PN WO200078817-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-EP005884.
XX
PR 23-JUN-1999; 99EP-0111994.
XX
PA (BOEH-) BOEHRINGER MANNHEIM GMBH.
XX
PI Jandrot-Perrus M;
XX
DR WPI; 2001-087141/11.
DR N-PSDB; AAP74994.
XX
CC Specific inhibitors of platelet collagen interactions and as a marker
CC for platelet age and platelet exposure to thrombotic and cardiovascular
CC disorders. GPVI is used for the manufacture of medicaments in the
CC therapeutic field of thrombotic and cardiovascular events, and disorders
CC related to platelet collagen interactions.
XX
SQ Sequence 419 AA;

Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

RESULT 4
AAB64273
ID AAB64273 standard; protein; 419 AA.
XX
AC AAB64273;
XX
DT 30-APR-2001 (first entry)
XX
DE Human IANG1 Z68-related protein #1.
XX
KW Human; IANG1 Z68; cardiatic cerebroprotective; cytostatic; anti-neoplastic;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO200078817-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-EP005884.
XX
PR 23-JUN-1999; 99US-0140308
PR 06-SEP-1999; 99US-0152424
PR 14-FEB-2000; 2000US-0182067
XX
PA (MILL-) MILLENNIUM PHARM INC
XX
PI Bastian S.E. Wilhelm S. Arnold P. Berrus M. Vollenbroeker W. Li S.
PI Qian M. Kingsbury G.
XX
DR WPI; 2001-087141/11.
DR N-PSDB; AAP74994.

```
XX
PT   New genes encoding human platelet expressed collagen receptor
PT   glycoprotein VI, and its modulators, useful for preventing, treating
PT   and diagnosing haemorrhagic disorders, thrombotic diseases and
PT   immunological disorders
XX
DT   Disclosure; Page 214; 214pp; English.
XX
CC   The present sequence is given in a specification relating to an isolated
CC   nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC   glycoprotein VI (GPVI), also called IAN5 2p8. The GPVI polypeptides
CC   and polypeptides and their modulators, e.g. antisense nucleic acids,
CC   ribozymes and antibodies, are useful for preventing, treating and
CC   diagnosing disorders associated with aberrant expression or activity of
CC   GPVI. These disorders include bleeding disorders
CC   (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC   (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC   disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC   ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC   infarction), immunological diseases (e.g. platelet disorders) and
CC   embryonic liver disorders. Preferably they are used to prevent acute
CC   cardiac ischaemia following angioplasty and metastatic cancers,
CC   especially of the colon and liver.
XX
SQ   Sequence  339 AA;

  Query Match             99.6%;  Score 99%;  DB 22;  Length 339;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-29;
  Matches  99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MPSQLVPFPWVMVLVSLVVLSGLVSLGSLHCVGFNLEAPQYLPYLQPGQNFSLRCHYKKE  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPSQLVPFPWVMVLVSLVVLSGLVSLGSLHCVGFNLEAPQYLPYLQPGQNFSLRCHYKKE  60

Qy      61 YFKTVKLFKERHRIEQTSGSQMVKSKYRLEHLSSRDAGSYWCRVEIPGLEEDEGTVELEL  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YFKTVKLFKERHRIEQTSGSQMVKSKYRLEHLSSRDAGSYWCRVEIPGLEEDEGTVELEL  120

Qy     121 HGVVPLQEPPLFMMMMVTSVVVVTTIVGSFVLLSFYVGLLFRDQKETMWPPNIPDPSKSH  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 HGVVPLQEPPLFMMMMVTSVVVVTTIVGSFVLLSFYVGLLFRDQKETMWPPNIPDPSKSH  180

Qy     181 IEQGLYFENSMTEFEDQSPFVGEELPAEPSGTLEEARTEFSLSTGNIQGNSTSQSK  239
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 IEQGLYFENSMTEFEDQSPFVGEELPAEPSGTLEEARTEFSLSTGNIQGNSTSQSK  239

RESULT 5
AAB61274
ID   AAB61274 standard; protein; 339 AA.
XX
AC   AAB61274;
XX
DT   01-APR-2003  (first entry)
XX
DE   Human IAN5 2p8 related protein #2.
XX
KW   Human; IAN5 2p8; cardiant; platelet aggregation; anti-thrombotic;
KW   thrombolytic; antiatherosclerotic; haemostatic; cytostatic; anti-GPVI;
KW   platelet membrane glycoprotein receptor; bleeding disorder;
KW   blood vessel injury; thrombotic disorder; haemorrhagic disorder;
KW   cerebrovascular; cardiovascular disease; immunological disorder;
KW   embryonic liver disorder.
XX
OS   Homo sapiens.
XX
PN   WO200218431-A1.
XX
PD   04-JAN-2002.
XX
PF   03-JUN-2001; 2001WO-US018152.
XX
PR   02-JUN-2000; 2000US-0208873P.
PR   08-DEC-2000; 2000US-0254124P.
PR   14-FEB-2001; 2001US-0268867P.
XX
PA   (MILL ) MILLENNIUM PHARM INC.
XX
PI   Bastian SJ, Vilcinskas L, Taylor Jones M, Vanderbeeken W, Gill JC;
PI   Glen MG, Kingsbury G;
XX
DR   WPI; 2002-208872/24.
DR   N-PSDB; AAF29487.
XX
PT   New genes encoding human platelet expressed collagen receptor,
PT   glycoprotein VI, and its modulators, useful for preventing, treating
PT   and diagnosing haemorrhagic disorders, thrombotic diseases and
PT   immunological disorders
XX
PS   Disclosure; Page 214; 214pp; English.
XX
CC   The present sequence is given in a specification relating to an isolated
CC   nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC   glycoprotein VI (GPVI), also called IAN5 2p8. The GPVI polypeptides
CC   and polypeptides and their modulators, e.g. antisense nucleic acids,
CC   ribozymes and antibodies, are useful for preventing, treating and
CC   diagnosing disorders associated with aberrant expression or activity of
CC   GPVI. These disorders include bleeding disorders
CC   (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC   (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC   disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC   ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC   infarction), immunological diseases (e.g. platelet disorders) and
CC   embryonic liver disorders. Preferably they are used to prevent acute
CC   cardiac ischaemia following angioplasty and metastatic cancers,
CC   especially of the colon and liver.
XX
SQ   Sequence  339 AA;

  Query Match             79.1%;  Score 264;  DB 22;  Length 339;
  Best Local Similarity   88.0%;  Pred. No. 2e-23;
  Matches  264;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy       1 MPSQLVPFPWVMVLVSLVVLSGLVSLGSLHCVGFNLEAPQYLPYLQPGQNFSLRCHYKKE  60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPSQLVPFPWVMVLVSLVVLSGLVSLGSLHCVGFNLEAPQYLPYLQPGQNFSLRCHYKKE  60

Qy      61 YFKTVKLFKERHRIEQTSGSQMVKSKYRLEHLSSRDAGSYWCRVEIPGLEEDEGTVELEL  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YFKTVKLFKERHRIEQTSGSQMVKSKYRLEHLSSRDAGSYWCRVEIPGLEEDEGTVELEL  120

Qy     121 HGVVPLQEPPLFMMMMVTSVVVVTTIVGSFVLLSFYVGLLFRDQKETMWPPNIPDPSKSH  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 HGVVPLQEPPLFMMMMVTSVVVVTTIVGSFVLLSFYVGLLFRDQKETMWPPNIPDPSKSH  180

Qy     181 IEQGLYFENSMTEFEDQSPFVGEELPAEPSGTLEEARTEFSLSTGNIQGNSTSQSK  239
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 IEQGLYFENSMTEFEDQSPFVGEELPAEPSGTLEEARTEFSLSTGNIQGNSTSQSK  239
```

```
AC   AAY74791;
XX
DT   04-APR-2001  (first entry)
XX
DE   Human IANP 2B3 extracellular domain.
XX
KW   Human; IANP2b-2B3; cardiant; cerebroprotective; glycoprotein VI;
KW   thrombolytic; antiatherosclerotic; haemostatic; GPVI; IANP;
KW   platelet membrane glycoprotein receptor; platelet aggregation;
KW   blood vessel injury; thrombotic disorder; haemorrhagic disorder;
KW   ischaemic cardiovascular disease; immunological disease;
KW   cancer.
XX
OS   Homo sapiens
XX
PN   WO200164717-A1.
XX
PD   04-JAN-2001.
XX
PF   30-JUN-2000;  2000WO-US018052.
XX
PR   30-JUN-1999;  99US-0141540P.
PR   06-OCT-1999;  99US-0158124P.
PR   14-FEB-2000;  2000US-0182667P.
XX
PA   (MILL ) MILLENNIUM PHARM INC.
XX
PI   Bastida SJ, Villoldo J, Jimenez Perez M, Vicente Perez A, Lopez MG, Kinassory G;
XX
DR   WPI; 2001-686779/79.
XX
PT   New DNA encoding human platelet expressed glycoprotein VI,
PT   glycoprotein VI, and its modulators, useful for preventing, treating and
PT   diagnosing haemorrhagic disorders, thrombotic disorders and
PT   cardiovascular diseases
XX
PS   Disclosure; Page 209 pp; 223pp; English.
XX
CC   The present sequence is given in a specification describing a platelet membrane
CC   nucleic acid molecule encoding a platelet membrane glycoprotein
CC   glycoprotein VI (GPVI), also called IANP 2b2, the GPVI protein, peptides
CC   and polypeptides and their modulators, e.g. antibodies, peptides,
CC   ribozymes and antibodies, are useful for preventing, treating and
CC   diagnosing disorders associated with platelet aggregation (e.g.
CC   GPVI. These disorders include bleeding disorders
CC   (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
CC   (e.g. thrombotic occlusion of the coronary arteries), cardiovascular
CC   disorders, coronary artery and cerebral artery stenosis (e.g. cerebral
CC   ischaemia), cardiovascular diseases (e.g. atherosclerosis, angina, cardiac
CC   infarction), immunological diseases (e.g. platelet disorders) and
CC   cytogenic liver disorders. Preferably they are used in prevention and
CC   cardiac ischaemia following angioplasty and restenosis
CC   especially of the colon and liver.
XX
SQ   Sequence  249 AA;

  Query Match             73.5%;  Score 249;  DB 22;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-22;
  Matches  249;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      21 QSGPGLVKPSETLSLTCTVSGGSVSSGSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVT 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 QSGPGLVKPSETLSLTCTVSGGSVSSGSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVT 64

Qy      85 SLAIGVPKNQFSLNLSSVTAADTAVYYCARDRGYSSGWYLEDYWGQGTLVTVSSASTKGPSVFPL 148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65 SLAIGVPKNQFSLNLSSVTAADTAVYYCARDRGYSSGWYLEDYWGQGTLVTVSSASTKGPSVFPL 128

Qy     149 LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS 212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     129 LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS 192

Qy     213 LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     193 LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP 256

Qy     277 EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     257 EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 320

Qy     341 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 404
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     321 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 384

Qy     405 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 464
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 444


RESULT 7
AAY74791
ID   AAY74791 standard; protein; 459 AA.
XX
AC   AAY74791;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Human GPVI external domain yeast alpha factor secreted.
XX
KW   Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
KW   vascular disease; thrombosis; plasmid pPICZGPVI; cardiovascular.
XX
OS   Chimeric - Saccharomyces cerevisiae.
OS   Chimeric - Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1..19
FT                   /label= Homo sapiens GPVI external_domain
FT                   /note= "corresponds to 21 aas residues of human
FT                   GPVI protein (AAY74791)"
FT   Region          447..459
FT                   /label= Myc epitope
FT   Region          464..609
FT                   /label= His tag
XX
PN   WO200181421-A1.
XX
PD   01-NOV-2001.
XX
PF   01-MAY-2001;  2001WO-US014125.
XX
PR   01-MAY-2000;  2000US-0201067P.
PR   08-AUG-2000;  2000US-0223982P.
XX
PA   (UNIV ) UNIV CINCINNATI.
XX
PI   Jandrot-Perrus M, Sun B, Nakamura T, Yamamoto N;
XX
DR   WPI; 2001-626701/71.
DR   N-PSDB; AAD02860.
XX
PT   Anti-thrombotic medicament, comprising a polypeptide having the
PT   extracellular domain of platelet membrane glycoprotein VI or its
PT   variant, useful for treating a vascular disease and reducing platelet
PT   activation
XX
PS   Disclosure; Fig 5; 74pp; English.
XX
CC   The present sequence is a chimeric protein encoded by pPICZGPVI
CC   DNA. The pPICZGPVI encodes human platelet membrane glycoprotein VI
CC   (GPVI) external domain, a yeast alpha factor secretion peptide and a
CC   histidine (His) tag. It is pPICZGPVI is used to produce a soluble
CC   recombinant (sr) GPVI. The sr-GPVI is useful for
CC   treating vascular disease, and for reducing platelet activation which
CC   involves contacting platelets with the medicament. The extracellular
CC   portion of GPVI is used therapeutically to attenuate platelet activation
CC   and aggregation and in treating thrombosis and other vascular diseases.
CC   Antibodies generated against GPVI are used as research and
CC   pharmacotherapeutic agents.
XX
SQ   Sequence  459 AA;

  Query Match             73.5%;  Score 249;  DB 22;  Length 459;
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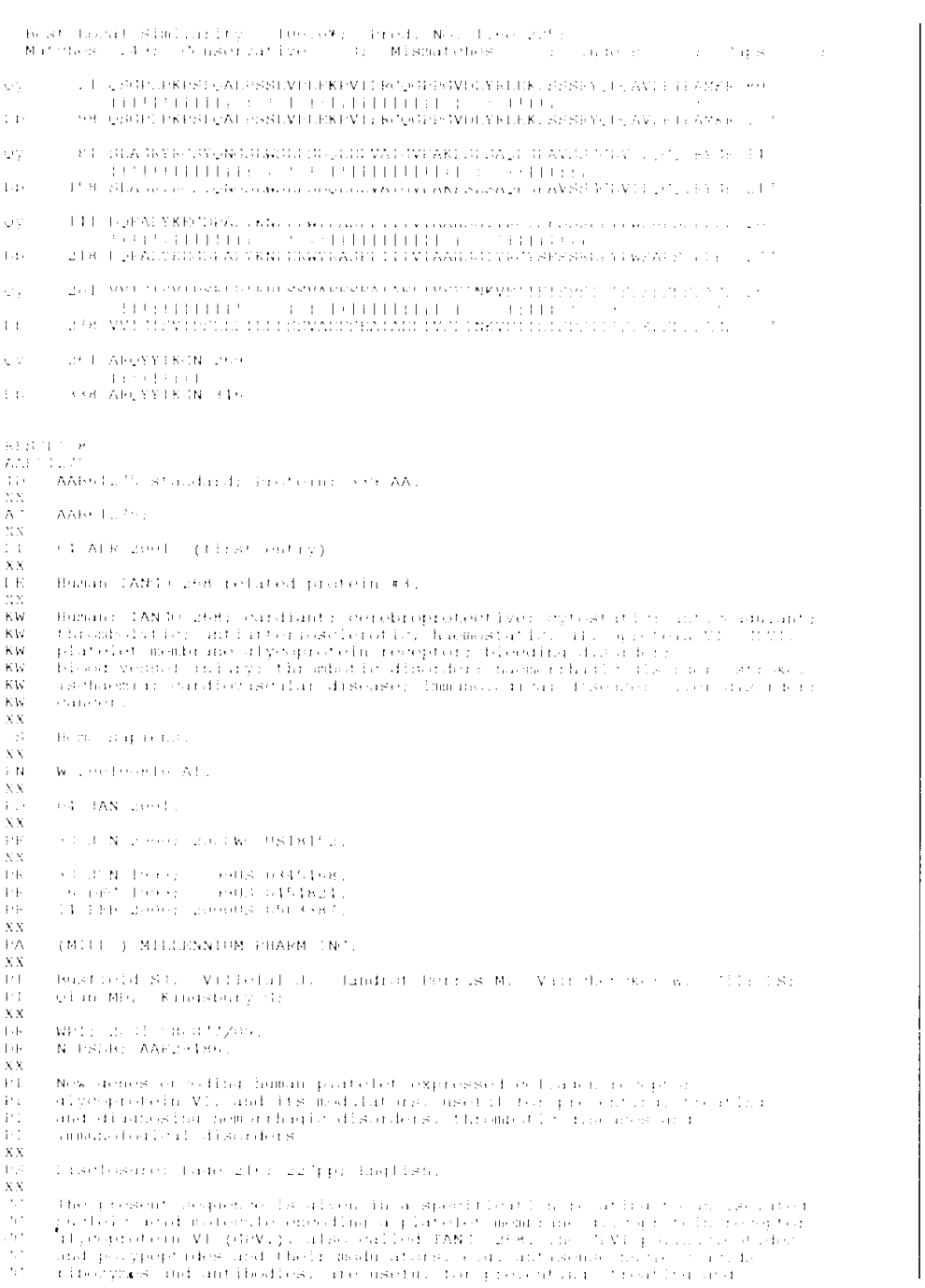
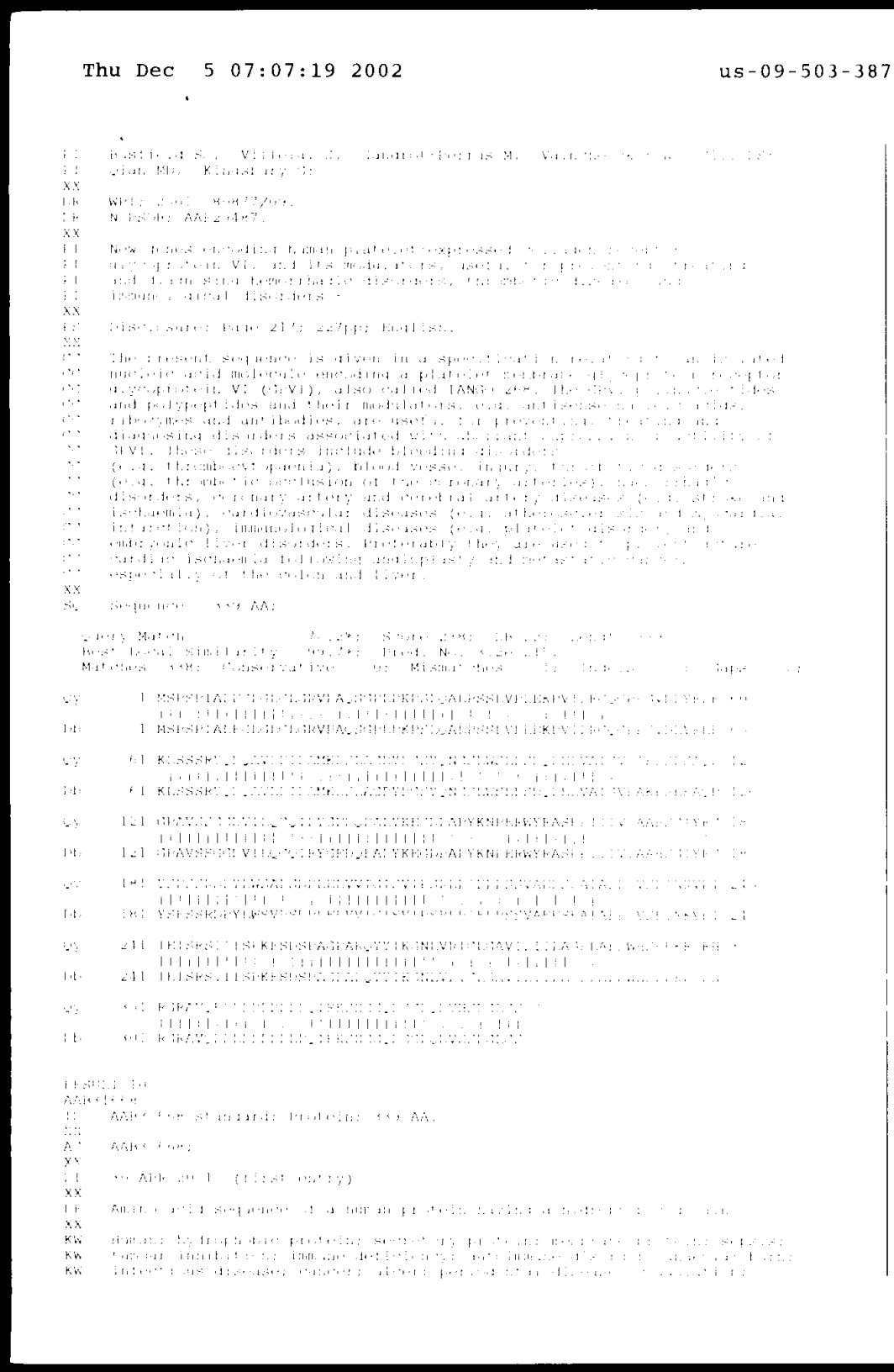
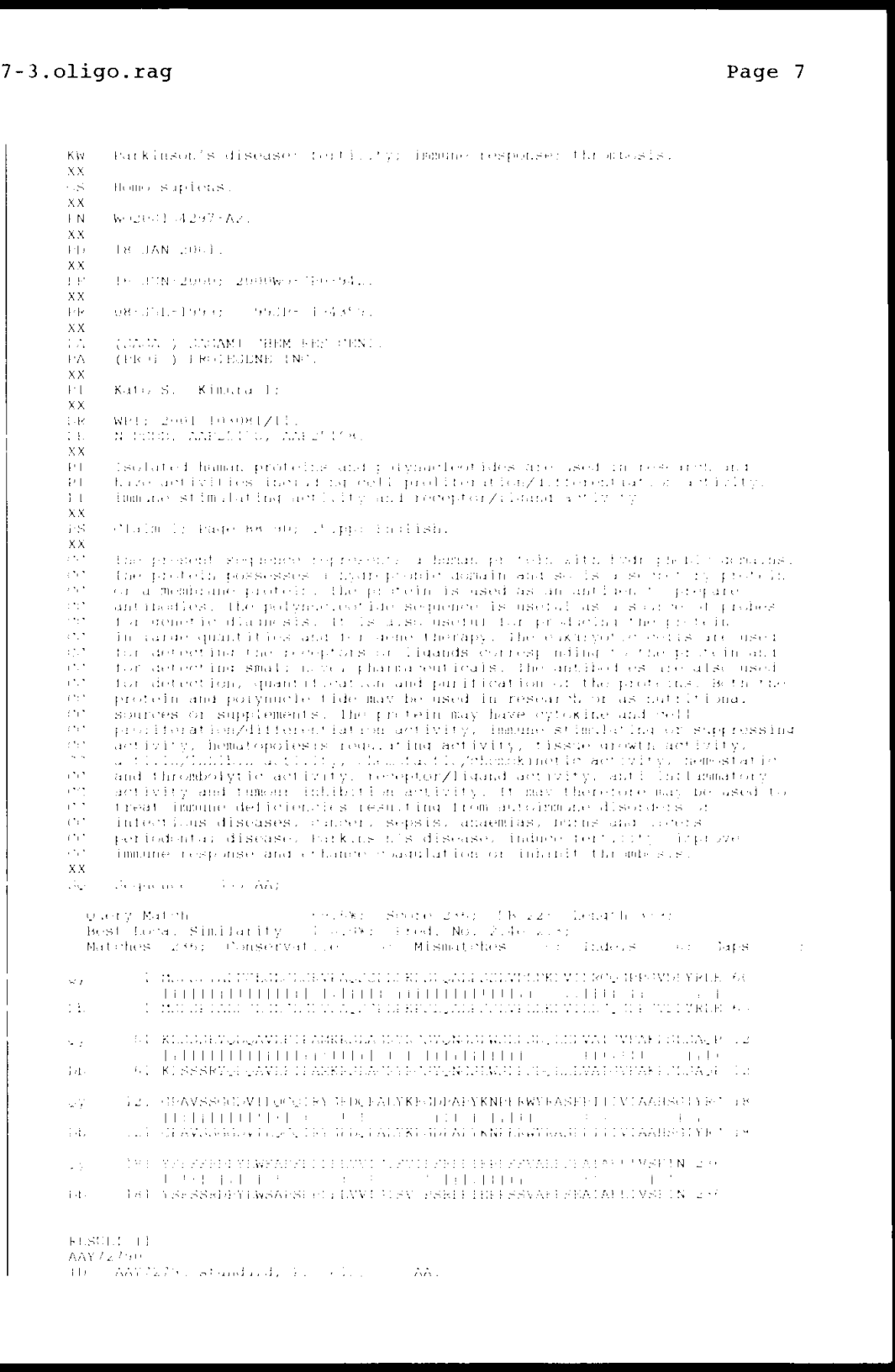


RESULT 9
AAB61_7
ID AAB61_7 standard; Protein; ??? AA.
XX
AC AAB61_7;
XX
DT 4-APR-2002 (first entry)
XX
DE Human IAN6 268 related protein #4.
XX
KW Human; IAN6 268; cardiant; cerebroprotective; cytostatic; antiviral;
KW thrombolytic; antiatherosclerotic; haemostatic; diagnostic; VEGF;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haematological disorder;
KW ischaemic cardiovascular disease; immunological disease; inflammation;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO200208281-A1.
XX
PD 31-JAN-2002.
XX
PF 26-JUL-2001; 2001WO-US023972.
XX
PR 26-JUL-2000; 2000US-0221078P.
PR 07-DEC-2000; 2000US-0251824P.
PR 14-FEB-2001; 2001US-0268987P.
XX
PA (MILL) MILLENNIUM PHARM INC.
XX
PI Bostrom SL, Vitolat JL, Landis Pettis M, Vitolat Rose W, Ellis CS;
PI Qiu MG, Kinnstary S;
XX
DR WPI; 2002-183772/24.
DR N-PSDB; AAB20496.
XX
PT New genes of cardiac human platelet expressed in large to specific
PT alpha-protein VI, and its modulators useful for prognosis, screening
PT and diagnosis of thrombotic disorders, thrombotic disorders and
PT immunological disorders.
XX
PS Disclosure; Page 216; 22pp; English.
XX
CC The present sequence is given in a specification to define novel human
CC platelet membrane-binding glycoprotein alpha-protein VI (GPV), also called IAN6 268, the GPVI protein and
CC and polypeptides and their modulators, e.g. antisense molecules,
CC ribozymes and antibodies, are useful for prognostic, screening and





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XX
AC   AAY74708;
XX
DT   01-MAY-2001  (first entry)
XX
DE   Human platelet membrane glycoprotein VI (GPVI).
XX
KW   Human platelet membrane glycoprotein VI; GPVI; fusion protein; Fc region;
KW   vascular disease; thrombosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_difference  1..74
FT                    /note= "Matches platelet membrane glycoprotein VI
FT                    (GPVI) protein"
FT   domain           1..74
FT                    /note= "Extracellular domain"
FT   misc_difference  1
FT                    /note= "Encoded by Ile"
FT   misc_difference  2
FT                    /note= "Encoded by Ala"
FT   misc_difference  3
FT                    /note= "Encoded by Thr"
FT   misc_difference  4
FT                    /note= "Encoded by Ser"
XX
PN   WO2001042451-A1.
XX
PD   14-JUN-2001.
XX
PF   11-DEC-2000; 2000WO-US033975.
XX
PR   11-DEC-1999;  99US-0170247.
PR   08-MAY-2000;  00US-0202951.
XX
PA   (SANK ) SANKYO CO LTD.
XX
PI   Tanaka N,  Sun B,  Nakamura T,  Yamamoto N;
XX
DR   WPI; 2001-422601/44.
DR   N-PSDB; AAQ02854.
XX
PT   Anti-thrombotic medicament, comprising a polypeptide having the
PT   extracellular domain of platelet membrane glycoprotein VI or its
PT   variant, useful for treating a vascular disease and reducing platelet
PT   activation
XX
PS   Claim 17; Fig 2; 46pp; English.
XX
CC   The present sequence is a human platelet membrane glycoprotein VI
CC   (GPVI). The medicament comprising GPVI is useful for treating
CC   vascular disease, and for reducing platelet activation which occurs
CC   contacting platelets with the medicament. The extracellular portion of
CC   GPVI is used therapeutically to attenuate platelet activation and
CC   aggregation and to treat thrombosis and other vascular diseases.
CC   Antibodies generated against GPVI are used as research and
CC   immunotherapeutic agents.
XX
SQ   Sequence   74 AA;

  Query Match             51.0%;  Score 174;  DB 2;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-54;
  Matches  74;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTIVIAAESIYSCYSFSSKEFEYTWSAPSSGSEEVVESVTFSEQDPEEAVAFTSEA 57
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 LTIVIAAESIYSCYSFSSKEFEYTWSAPSSGSEEVVESVTFSEQDPEEAVAFTSEA 57

Qy     58 IAIGIVSFINKVSTIFFSVTIKKLQLSIASLPVYEMNVEFTSAVTLIASI 107
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     58 IAIGIVSFINKVSTIFFSVTIKKLQLSIASLPVYEMNVEFTSAVTLIASI 107


RESULT 12
AAY74708
ID   AAY74708 standard; protein; 74 AA.
XX
AC   AAY74708;
XX
DT   01-MAY-2001  (first entry)
XX
DE   Human platelet membrane glycoprotein VI (GPVI) partial protein #1
XX
KW   Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
KW   vascular disease; thrombosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_difference  1
FT                    /note= "Encoded by 'Y'"
XX
PN   WO200104251-A1.
XX
PD   18-JAN-2001.
XX
PF   11-DEC-2000; 2000WO-US033975.
XX
PR   11-DEC-1999;  99US-0170247.
PR   08-MAY-2000;  00US-0202951.
XX
PA   (SANK ) SANKYO PHARM CO LTD.
XX
PI   Tanaka N,  Sun B,  Nakamura T,  Yamamoto N;
XX
DR   WPI; 2001-422601/44.
DR   N-PSDB; AAQ02854.
XX
PT   Anti-thrombotic medicament, comprising a polypeptide having the
PT   extracellular domain of platelet membrane glycoprotein VI or its
PT   variant, useful for treating a vascular disease and reducing platelet
PT   activation
XX
PS   Claim 17; Fig 2; 46pp; English.
XX
CC   The present sequence is a human platelet membrane glycoprotein VI (GPVI)
CC   partial protein #1. The medicament comprising GPVI is useful for treating
CC   vascular disease, and for reducing platelet activation which occurs
CC   contacting platelets with the medicament. The extracellular portion of
CC   GPVI is used therapeutically to attenuate platelet activation and
CC   aggregation and to treat thrombosis and other vascular diseases.
CC   Antibodies generated against GPVI are used as research and
CC   immunotherapeutic agents.
XX
SQ   Sequence   74 AA;

  Query Match             19.8%;  Score 67;  DB 2;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-15;
  Matches  67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTIVIAAESIYSCYSFSSKEFEYTWSAPSSGSEEVVESVTFSEQDPEEAVAFTSEA 57
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 LTIVIAAESIYSCYSFSSKEFEYTWSAPSSGSEEVVESVTFSEQDPEEAVAFTSEA 57

Qy     58 IAIGIVS 64
          ||||||| ||
Db     58 IAIGIVS 64
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```
RESULT 13
AAY72[illegible]
ID   AAY72[illegible] standard; Protein; 74 AA.
XX
AC   AAY72[illegible];
XX
DT   [illegible] MAY 2001  (first entry)
XX
DE   Human platelet membrane glycoprotein VI (GPVI) partial [illegible]
XX
KW   Human; platelet membrane glycoprotein VI; GPVI; [illegible] therapy;
KW   vascular disease; thrombosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 15
FT                   /note= "Encoded by [illegible]"
XX
PN   WO2001[illegible] A1.
XX
PD   [illegible] MAR 2001.
XX
PF   [illegible] SEP 2000; 2000WO-[illegible].
XX
PR   [illegible] SEP-1999;   99US-0152[illegible].
PR   [illegible]-1999;   99US-0158[illegible].
XX
PA   (SUKA ) [illegible]SUKA PHARM CO LTD.
XX
PI   Tandon N,  Sun B,  Nakamura I,  Yamamoto N;
XX
DR   WPI; 2001-22[illegible]/23.
DR   N-PSDB; AAD[illegible].
XX
PT   Anti-thrombotic medicament, comprising a polypeptide [illegible]
PT   extracellular domain of platelet membrane glycoprotein VI or [illegible]
PT   variant, useful for treating a vascular disease and [illegible] platelet
PT   activation -
XX
PS   Disclosure; Fig 2; 74pp; English.
XX
CC   The present sequence is a human platelet membrane glycoprotein VI (GPVI)
CC   partial protein #b. The medicament comprising GPVI is useful for treating
CC   vascular disease, and for reducing platelet activation which involves
CC   contacting platelets with the medicament. The extracellular portion of
CC   GPVI is used therapeutically to attenuate platelet activation and
CC   aggregation and to treat thrombosis and other vascular diseases.
CC   Antibodies generated against GPVI are used as research and
CC   immunotherapeutic agents.
XX
SQ   Sequence   74 AA;

  Query Match             15.[illegible]%;  Score 52;  DB 22;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-41;
  Matches   52;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        16 GRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLEKLSSSRY [illegible]
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        16 GRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLEKLSSSRY [illegible]


RESULT 14
AAB61262
ID   AAB61262 standard; Protein; 51 AA.
XX
AC   AAB61262;
XX
DT   04 APR 2001  (first entry)
XX
DE   Human TANGO 268 cytoplasmic domain.
XX
KW   Human; TANGO 268; cardiant; cerebroprotective; cytostatic; [illegible]
KW   thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW   platelet membrane glycoprotein receptor; bleeding disorder;
KW   blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW   ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW   cancer.
XX
OS   Homo sapiens.
XX
PN   WO200100810 A1.
XX
PD   04 JAN 2001.
XX
PF   30 JUN 2000; 2000WO-US18[illegible].
XX
PR   30 JUN-1999;   99US-0[illegible].
PR   06 DEC-1999;   99US-0[illegible]1824.
PR   14 FEB-2000; 2000US-0[illegible].
XX
PA   (MILL ) MILLENNIUM PHARM INC.
XX
PI   Busfield SJ,  Villeval [illegible],  Gaudrot-Perrus M,  Vainchenker W,  [illegible]
PI   Glan MP,  Kingsbury G;
XX
DR   WPI; 2001-080977/09.
XX
PT   New genes encoding human platelet expressed [illegible] receptor,
PT   glycoprotein VI, and its modulators, useful for preventing, treating
PT   and diagnosing hemorrhagic disorders, thrombotic diseases and
PT   immunological disorders
XX
PS   Disclosure; Page 204; 127pp; English.
XX
CC   The present sequence is given in a specification relating to an isolated
CC   nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC   glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC   and polypeptides and their modulators, e.g. antisense nucleic acids,
CC   ribozymes and antibodies, are useful for preventing, treating and
CC   diagnosing disorders associated with aberrant expression or activity of
CC   GPVI. These disorders include bleeding disorders
CC   (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC   (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC   disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC   ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC   infarction), immunological diseases (e.g. platelet disorder) and
CC   embryonic liver disorders. Preferably they are used to prevent acute
CC   cardiac ischaemia following angioplasty and metastatic cancers,
CC   especially of the colon and liver.
XX
SQ   Sequence   51 AA;

  Query Match             [illegible]%;  Score 51;  DB 22;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 4e-41;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       289 [illegible]VHSPGLGS [illegible]
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 [illegible]VHSPGLGS 51


RESULT 15
AAB61259
ID   AAB61259 standard; Protein; 37 AA.
XX
AC   AAB61259;
XX
DT   04 APR 2001  (first entry)
XX
DE   Human TANGO 268 Ig like domain #2.
XX
KW   Human; TANGO 268; cardiant; cerebroprotective; cytostatic; antiarteriosclerotic;
KW   thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW   platelet membrane glycoprotein receptor; bleeding disorder;
KW   blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
```

KW ischaemic cardiovascular disease; cardiovascular disease;
KW stroke.
XX
OS Homo sapiens.
XX
PN WO0168676-A1.
XX
PD 20-SEP-2001.
XX
PF 16-MAR-2000; 2001WO-US08152.
XX
PR 16-MAR-1999; 99US-0124948.
PR 16-SEP-1999; 99US-0154084.
PR 14-FEB-2000; 2000US-0503087.
XX
PA (MILL) MILLENNIUM PHARM INC.
XX
PI Bostield SJ, Vilbrax S, Jandrot Perrus M, Vanbelzen W, Gill DC;
PI Glan MG, Kinsbury S;
XX
DR WPI; 2001-608677/69.
XX
PT New notes encoding human platelet expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders
XX
PS Disclosure; Page 253; 227pp; English.
XX
CC The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called IAN8- 268. The GPVI polypeptides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
SQ Sequence 41 AA;

Query Match 12.1%; Score 47; DB 22; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.00;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 YQQPPSVEGYKLEKLSSSEYQLPAVELIAMKESLAGPYP 86
||||||||||||||||||||||||||||||||||||||||||
Db 1 YQQPPSVEGYKLEKLSSSEYQLPAVELIAMKESLAGPYP 41

RESULT 12
AAB61268
ID AAB61268 standard; protein; 27 AA.
XX
AC AAB61268;
XX
DT 01-APR-2001 (first entry)
XX
DE Mouse IAN8- 268 extracellular domain.
XX
KW Mouse; IAN8- 268; cardiant; cerebrospecific; cytostatic; anticonvulsant;
KW thrombolytic; antiatherosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemic cardiovascular disease; immunodermal disease; liver disorder;
KW cancer.
XX
OS Mus musculus.
XX
PN WO0168676-A1.

XX
RL 1 JAN 2001
XX
RF <...JUN 2000; 2000WO-US016172.
XX
RP 30-JUN-1999; 99US-0341568.
RP 06-DEC-1999; 99US-0169424.
RR 14-FEB-2000; 2000US-0503387.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Postigli AE, Villoldo J, Zanardo Berros M, Valenzuela W, Olivares
PI Glan MD, Kingsbury S
XX
DR WPI; 2001-080877/09.
XX
PT New genes encoding human platelet-expressed collagen receptor
PT glycoprotein VI, and its modulators, useful for prevention, treatment
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders
XX
PS Disclosure; Fig 7; 227pp; English.
XX
CC The present sequence is given in a specification which identifies and
CC isolates novel nucleic acid molecule encoding a platelet membrane type protein termed
CC glycoprotein VI (GPVI), also called IAN8. The GPVI polypeptides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemostatic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
SQ Sequence 292 AA;

Query Match 96.2%; Score 21; DB 22; Length 292;
Best Local Similarity 1.00%; Pred. No. 2.7e+11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFTLIVIAAHSGIYFCYSFSS 21
EFTLIVIAAHSGIYFCYSFSS
Db 143 EFTLIVIAAHSGIYFCYSFSS 163

RESULT 19
AAB91267
ID AAB91267 standard; protein; 292 AA.
XX
AC AAB91267;
XX
DT 04-APR-2001 (first entry)
XX
DE Mouse IAN8 268 protein.
XX
KW Mouse; IAN8 268; cardiant; cerebroprotective; CVS; stroke; anti-apoptotic;
KW thrombolytic; antiatherosclerotic; haemostatic; dyslipidaemic; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemostatic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Mus musculus.
XX
RN [1]
XX
RA -Postigli A.E.;
XX
RT ;
XX
RL Submitted (04-JAN-2001) to the EMBL/GenBank/DDBJ databases.
XX
RP 1-292
XX
RA -Postigli A.E., Villoldo J., Zanardo Berros M., Valenzuela W.,
RA Olivares Glanville S., Kingsbury S.;
RT "Novel genes encoding human platelet-expressed collagen receptor
RT glycoprotein VI, and its modulators, useful for prevention, treatment
RT and diagnosing hemorrhagic disorders, thrombotic diseases and
RT immunological disorders";
RL Patent number WO0116172-A1/1, 08-MAR-2001;
RL 30-JUN-2000; 2000WO-US016172.
XX
RP 1-292
XX
RA -Postigli A.E., Villoldo J., Zanardo Berros M., Valenzuela W.,
RA Olivares Glanville S., Kingsbury S.;
RT "Novel genes encoding human platelet-expressed collagen receptor
RT glycoprotein VI, and its modulators, useful for prevention, treatment
RT and diagnosing hemorrhagic disorders, thrombotic diseases and
RT immunological disorders";
RL Patent number WO0116172-A1/1, 08-MAR-2001;
RL 30-JUN-1999; 99US-0341568.
RL 06-DEC-1999; 99US-0169424.
RL 14-FEB-2000; 2000US-0503387.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Postigli AE, Villoldo J, Zanardo Berros M, Valenzuela W, Olivares
PI Glan MD, Kingsbury S
XX
DR WPI; 2001-080877/09.
XX
PT New genes encoding human platelet-expressed collagen receptor
PT glycoprotein VI, and its modulators, useful for prevention, treatment
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders
XX
PS Disclosure; Fig 7; 227pp; English.
XX
CC The present sequence is given in a specification which identifies and
CC isolates novel nucleic acid molecule encoding a platelet membrane type protein termed
CC glycoprotein VI (GPVI), also called IAN8. The GPVI polypeptides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemostatic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
SQ Sequence 292 AA;

Query Match 96.2%; Score 21; DB 22; Length 292;
Best Local Similarity 1.00%; Pred. No. 2.7e+11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFTLIVIAAHSGIYFCYSFSS 21
EFTLIVIAAHSGIYFCYSFSS
Db 143 EFTLIVIAAHSGIYFCYSFSS 163

RESULT 19
AAB91267
ID AAB91267 standard; protein; 292 AA.
XX
AC AAB91267;
XX
DT 04-APR-2001 (first entry)
XX
DE Mouse IAN8 268 protein.
XX
KW Mouse; IAN8 268; cardiant; cerebroprotective; CVS; stroke; anti-apoptotic;
KW thrombolytic; antiatherosclerotic; haemostatic; dyslipidaemic; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemostatic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Mus musculus.
XX
RN [1]
XX
RA -Postigli A.E.;
XX
RT ;
XX
RL Submitted (04-JAN-2001) to the EMBL/GenBank/DDBJ databases.
XX
RP 1-292
XX
RA -Postigli A.E., Villoldo J., Zanardo Berros M., Valenzuela W.,
RA Olivares Glanville S., Kingsbury S.;
RT "Novel genes encoding human platelet-expressed collagen receptor
RT glycoprotein VI, and its modulators, useful for prevention, treatment
RT and diagnosing hemorrhagic disorders, thrombotic diseases and
RT immunological disorders";
RL Patent number WO0116172-A1/1, 08-MAR-2001;
RL 30-JUN-2000; 2000WO-US016172.
XX
RP 1-292
XX
RA -Postigli A.E., Villoldo J., Zanardo Berros M., Valenzuela W.,
RA Olivares Glanville S., Kingsbury S.;
RT "Novel genes encoding human platelet-expressed collagen receptor
RT glycoprotein VI, and its modulators, useful for prevention, treatment
RT and diagnosing hemorrhagic disorders, thrombotic diseases and
RT immunological disorders";
RL Patent number WO0116172-A1/1, 08-MAR-2001;
RL 30-JUN-1999; 99US-0341568.

```
PN   6,[illegible]
PD   24-FEB-2[illegible]
XX
PA   (MILL ) MILLENNIUM PHARM INC.
XX
PI   Bonfield S.L.  Villegal I.  Jandrot Perrus M.  Vitaliano K.  S.L.S.
PI   Qian M.  Kinsbury S.
XX
DR   WPI; 2001-[illegible]
DR   N-PSDB; AAE29[illegible]
XX
PT   New genes encoding human platelet expressed collagen receptor,
PT   glycoprotein VI, and its modulators, useful for prevention, treatment
PT   and diagnosing hemorrhagic disorders, thrombotic disease and
PT   immunological disorders
XX
PS   Disclosure; Page 238 pp; 227pp; English.
XX
CC   The present sequence is given in a specification relating to an isolated
CC   nucleic acid molecule encoding a platelet membrane glycoprotein referred to
CC   glycoprotein VI (GPVI), also called IAN#2 268. The GPVI polynucleotides
CC   and polypeptides and their modulators, e.g. antisense nucleic acids,
CC   ribozymes and antibodies, are useful for prevention, treating and
CC   diagnosing disorders associated with aberrant expression or activity of
CC   GPVI. These disorders include bleeding disorders
CC   (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
CC   (e.g. thrombotic occlusion of the coronary arteries), hemostatic
CC   disorders, coronary artery and cerebral artery disease (e.g. stroke and
CC   ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC   infarction), immunological diseases (e.g. platelet disorder) and
CC   embryonic liver disorders. Preferably they are used to prevent acute
CC   cardiac ischaemia following angioplasty and metastatic cancers
CC   especially of the colon and liver.
XX
SQ   Sequence  313 AA;

  Query Match             [illegible]%; Score 21; DB 22; Length 313;
  Best Local Similarity   [illegible]%; Pred. No. 2.6e-[illegible];
  Matches   21; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Qy      195 FPTCIVIAAHLSIYP*YSPSS 215
            ||||||||||||||||||||
Db      149 FPTCIVIAAHLSIYP*YSPSS 169


RESULT 20
AAB61278
ID   AAB61278 standard; Protein; 313 AA.
XX
AC   AAB61278;
XX
DT   04-APR-2001  (first entry)
XX
DE   Mouse IAN#2 268 related protein #1.
XX
KW   Human; IAN#2 268; cardiant; cerebroprotective; cytostatic; anti-restenotic;
KW   thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW   platelet membrane glycoprotein receptor; bleeding disorder;
KW   blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW   ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW   cancer.
XX
OS   Mus musculus.
XX
PN   WO200153463-A1.
XX
PD   04-JAN-2001.
XX
PF   20-JUN-2000; 2000WO-US016724.
XX
PR   [illegible]-JUN-1999;  99US-0141849.
PR   [illegible]-DEC-1999;  99US-0454621.
PR   24-FEB-2000; 2000US-0514398.
XX
PA   (MILL ) MILLENNIUM PHARM INC.
XX
PI   Bonfield S.L.  Villegal I.  Jandrot Perrus M.  Vitaliano K.  S.L.S.
PI   Qian M.  Kinsbury S.
XX
DR   WPI; 2001-[illegible]
DR   N-PSDB; AAE29[illegible]
XX
PT   New genes encoding human platelet expressed collagen receptor,
PT   glycoprotein VI, and its modulators, useful for prevention, treatment
PT   and diagnosing hemorrhagic disorders, thrombotic disease and
PT   immunological disorders
XX
PS   Disclosure; Page 238 pp; 227pp; English.
XX
CC   The present sequence is given in a specification relating to an isolated
CC   nucleic acid molecule encoding a platelet membrane glycoprotein referred to
CC   glycoprotein VI (GPVI), also called IAN#2 268. The GPVI polynucleotides
CC   and polypeptides and their modulators, e.g. antisense nucleic acids,
CC   ribozymes and antibodies, are useful for prevention, treating and
CC   diagnosing disorders associated with aberrant expression or activity of
CC   GPVI. These disorders include bleeding disorders
CC   (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
CC   (e.g. thrombotic occlusion of the coronary arteries), haemostatic
CC   disorders, coronary artery and cerebral artery disease (e.g. stroke and
CC   ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC   infarction), immunological diseases (e.g. platelet disorder) and
CC   embryonic liver disorders. Preferably they are used to prevent acute
CC   cardiac ischaemia following angioplasty and metastatic cancers
CC   especially of the colon and liver.
XX
SQ   Sequence  313 AA;

  Query Match             [illegible]%; Score 21; DB 22; Length 313;
  Best Local Similarity   [illegible]%; Pred. No. 2.6e-[illegible];
  Matches   21; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Qy      195 FPTCIVIAAHLSIYP*YSPSS 215
            ||||||||||||||||||||
Db      149 FPTCIVIAAHLSIYP*YSPSS 169


RESULT 21
AAB61278
ID   AAB61278 standard; Protein; 313 AA.
XX
AC   AAB61278;
XX
DT   04-APR-2001  (first entry)
XX
DE   Mouse IAN#2 268 related protein #2.
XX
KW   Human; IAN#2 268; cardiant; cerebroprotective; cytostatic; anti-restenotic;
KW   thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW   platelet membrane glycoprotein receptor; bleeding disorder;
KW   blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW   ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW   cancer.
XX
OS   Mus musculus.
XX
PN   WO200153463-A1.
XX
PD   04-JAN-2001.
XX
PF   20-JUN-2000; 2000WO-US016724.
XX
PR   [illegible]-JUN-1999;  99US-0141849.
PR   [illegible]-DEC-1999;  99US-0454621.
PR   24-FEB-2000; 2000US-0514398.
XX
PA   (MILL ) MILLENNIUM PHARM INC.
```

XX
PT Posfield S.L. Villette J. Gaudet Bertrand M. Vaterbeuker W. [illegible]
PT Qian M., Kinasbury C.
XX
PN WO: 2001 000877/04.
PD 4-JAN-2001.
XX
PF New genes encoding human platelet expressed antigens termed
PF glycoprotein VI, and its modulators, useful for treating
PF and diagnosing hemorrhagic disorders, thrombotic diseases and
PF immunological disorders.
XX
PS Disclosure; Page 229 [illegible] pp; English.
XX
CC The present sequence is taken from a specification describing an isolated
CC particle acid molecule encoding a platelet membrane glycoprotein
CC glycoprotein VI (GPVI), also called IAN9 268. The GPVI polypeptides
CC and polypeptides and their modulators, e.g. antisense, ribozyme,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression of GPVI,
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent adverse
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
SQ Sequence 413 AA;

Query Match 0.2%; Score 2; DB 22; Length 413;
Best Local Similarity 50.0%; Pred. No. 2.9e+11;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 PPCTIVIAARSGIYSCYGESS 187
:: :
Db 166 PLCTIVIAARSGIYSCYSESS 188

RESULT 22
AAB61284
ID AAB61284 standard; protein; 413 AA.
XX
AC AAB61284;
XX
DT 04-APR-2001 (first entry)
XX
DE Mouse IAN9 268-related protein #4.
XX
KW Human; IAN9 268; cardiac; cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiatherosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Mus musculus.
XX
PN WO200100816-A1.
XX
PD 04-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-US017842.
XX
PR 30-JUN-1999; 99US-0341808.
PR 06-OCT-1999; 99US-0158218.
PR 14-FEB-2000; 2000US-0504687.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Posfield S.L., Villette J., Gaudet Bertrand M., Vaterbeuker W., Qian M.,
PI Kinasbury C.
XX

```
DE   WO 2002077027-A1.
DE   New genes encoding human platelet expressed cell surface receptor
DE   glycoprotein VI, and its modulators, useful for prevention, treatment
DE   and diagnosing haemorrhagic disorders, thrombotic diseases and
DE   immunological disorders
XX
PD   Document Type: Patent; 227pp; English.
XX
CC   The present sequence is given in a specification relating to an isolated
CC   nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC   glycoprotein VI (GPVI), also called IAN50 208. The GPVI polypeptides,
CC   and polypeptides and their modulators, e.g. antisense nucleic acids,
CC   ribozymes and antibodies, are useful for prevention, treatment and
CC   diagnosing disorders associated with aberrant expression or activity of
CC   GPVI. These disorders include bleeding disorders
CC   (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC   (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC   disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC   ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC   infarction), immunological diseases (e.g. platelet disorder) and
CC   embryonic liver disorders. Preferably they are used to prevent acute
CC   cardiac ischaemia following angioplasty and metastatic cancers,
CC   especially of the colon and liver.
XX
SQ   Sequence   23 AA;

  Query Match             9.2%;  Score 23;  DB 22;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MSDSPIALPCIGAGPVFA 20
           |||||||||||||||||||
Db       1 MSDSPIALPCIGAGPVFA 20

RESULT 24
AAB64940
ID   AAB64940 standard; peptide; 20 AA.
XX
AC   AAB64940;
XX
DT   07-MAR-2001  (first entry)
XX
DE   Human glycoprotein VI leader sequence.
XX
KW   Human; thrombolytic; cardiac glycoprotein VI; GPVI;
KW   platelet membrane glycoprotein; platelet activation;
KW   platelet collagen interaction; thrombotic disorder;
KW   cardiovascular disorder.
XX
OS   Homo sapiens.
XX
PN   WO200077027-A1.
XX
PD   14-DEC-2000.
XX
PF   25-APR-2000; 2000WO-EP03804.
XX
PR   27-MAY-1999;  99GB-0012094.
XX
PA   (MERE ) MERCK PATENT GMBH
XX
PI   Clemetson KJ;
XX
DR   WPI; 2001-092494/01.
DR   N-PSDB; AAC84980.
XX
PT   Recombinant human glycoprotein VI, useful for treating thrombotic,
PT   cardiovascular diseases or platelet surface interactions
XX
PS   Claim 4; Fig 1; 27pp; English.
XX
CC   The present sequence is the leader sequence for human glycoprotein VI
CC   (GPVI). GPVI is a platelet membrane glycoprotein which forms a complex

RESULT 25
AAB64942
ID   AAB64942 standard; peptide; 20 AA.
XX
AC   AAB64942;
XX
DT   07-MAR-2001  (first entry)
XX
DE   Human glycoprotein VI leader sequence.
XX
KW   Human; thrombolytic; cardiac glycoprotein VI; GPVI;
KW   platelet membrane glycoprotein; platelet activation;
KW   platelet collagen interaction; thrombotic disorder;
KW   cardiovascular disorder.
XX
OS   Homo sapiens.
XX
PN   WO200077027-A1.
XX
PD   14-DEC-2000.
XX
PF   25-APR-2000; 2000WO-EP03804.
XX
PR   27-MAY-1999;  99GB-0012094.
XX
PA   (MERE ) MERCK PATENT GMBH
XX
PI   Clemetson KJ;
XX
DR   WPI; 2001-092494/01.
DR   N-PSDB; AAC84980.
XX
PT   Recombinant human glycoprotein VI, useful for treating thrombotic,
PT   cardiovascular diseases or platelet surface interactions
XX
PS   Claim 4; Fig 1; 27pp; English.
XX
CC   The present sequence is the leader sequence for human glycoprotein VI
CC   (GPVI). GPVI is a platelet membrane glycoprotein which forms a complex
```

Query Match 5.9%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFS 4
|||| |
Db 1 MSFS 4

RESULT 26
AAB61641
ID AAB61641 standard; protein; 4 AA.
XX
AC AAB61641;
XX
DT 14-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #48442.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; DNA probe;
KW food supplement; medical imaging; diagnostic; neural disease;
KW
OS Homo sapiens
XX
PN WO200208437-A2.
XX
PD 31-JAN-2002.
XX
PF 24-JUL-2001; 2001WO-US023417.
XX
PR 27-JUL-2000; 2000US-0221217.
PR 28-AUG-2000; 2000US-0228042.
XX
PA (HYSE) HYSEQ INC.
XX
PI Tribouley C, Lal P, Tang YT;
XX
DR WPI; 2002-183691/24.
DR N-PSDB; AAB61640.
XX
PT New isolated polynucleotide and encoded polypeptide useful in
PT diagnostics, therapeutics, gene mapping, identification of genes
PT responsible for genetic disorders or other traits, and in assays
PT for biodiversity -
XX
PS Claim 26; SEQ ID NO 45200; 1498pp; English.
XX
CC The invention relates to isolated polynucleotide (I), and
CC polypeptide (II) sequences. (I) is useful as hybridization probes,
CC polymerase chain reaction (PCR) primers, antisense molecules,
CC and gene mapping, and in recombinant production. (I) and
CC polynucleotides are also used in diagnostics to express peptides
CC for identifying expressed genes. (II) is used in binding assays for
CC testing the ligand activity of (II) or related fusion proteins. (II)
CC (a), (II) is useful for determining antibodies raised against (II) or
CC quantitating a polypeptide in tissue, as molecular weight markers and
CC a food supplement. (II) and its binding partners are useful in
CC inducing cell sites expressing (II). (I) and (II) are useful in treating
CC disorders involving aberrant protein expression or activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of genes
CC responsible for genetic disorders or other traits, assays for viral,
CC and to provide other types of data and products dependent on DNA and

CC amino acid sequences. AB2p to AB2p5127 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp://ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4 AA;

Query Match 5.9%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFS 4
|||| |
Db 1 MSFS 4

RESULT 27
AAB61640
ID AAB61640 standard; protein; 4 AA.
XX
AC AAB61640;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human IAN10 268 transmembrane domain.
XX
KW Human; IAN10 268; central nervous system; cytostatic; antineoplastic;
KW thrombolytic; antiatherosclerotic; antihaemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disorder; liver disorder;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO200208437-A2.
XX
PD 31-JAN-2002.
XX
PF 24-JUL-2001; 2001WO-US023417.
XX
PR 27-JUL-2000; 2000US-0221217.
PR 28-AUG-2000; 2000US-0228042.
XX
PA (HYSE) HYSEQ INC.
XX
PI Tribouley C, Lal P, Tang YT;
XX
DR WPI; 2002-183691/24.
DR N-PSDB; AAB61641.
XX
PT New genes encoding human platelet expressed glycoprotein receptor,
PT glycoprotein VI, and its modulators, useful in preventing, treating
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders -
XX
PS Disclosure; Page 2887; 2979pp; English.
XX
CC The present sequence is novel in a specific sense relative to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI) also called IAN10 268. The GPVI polypeptides
CC and polypeptides and GPVI activators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and peripheral
CC infection), immunological diseases (e.g. platelet disorder) and
CC hepatocyte liver disorders. Preferably they are used to prevent or

```
XX   ...ovular ischaemic follicular meningitis and/or ...
XX   ...especially of the colon and liver.
XX
SQ   Sequence  ... AA;

  Query Match                 ...%;  Score ...;  DB 22;  Length ...;
  Best Local Similarity   ...%;  Pred. No. ...e-...;
  Matches  ...;  Conservative  ...;  Mismatches  ...;  Indels  ...;  Gaps  ...;

Qy      ... IVRETGSAVIIILAVFLA ...
            ||| | |||||| | | |
Db        1 IVRETGSAVIIILAVFLA 19


RESULT 28
AAY72815
ID   AAY72815 standard; peptide; 19 AA.
XX
AC   AAY72815;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Human platelet membrane glycoprotein VI (GPVI) peptide 11.
XX
KW   Human; platelet membrane glycoprotein VI; GPVI; thrombocytic disorder;
KW   vascular disease; thrombosis.
XX
OS   Homo sapiens.
XX
PN   WO200158421-A1.
XX
PD   09-AUG-2001.
XX
PF   01-SEP-2000; 2000WO-US024075.
XX
PR   01-SEP-1999;  1999US-152217P.
PR   08-OCT-1999;  1999US-158427P.
XX
PA   (GENA ) GENAERA INVEST BV.
XX
PI   Lenden N;  Sun B;  Nakamura I;  Yamamoto N;
XX
DR   WPI; 2001-522691/56.
XX
PT   Anti-thrombotic medicament, comprising a polypeptide having the
PT   extracellular domain of platelet membrane glycoprotein VI or its
PT   variant, useful for treating a vascular disease and reducing platelet
PT   activation.
XX
PS   Claim 13; Page 58; 74pp; English.
XX
CC   The present sequence is a human platelet membrane glycoprotein VI (GPVI)
CC   peptide 11. The medicament comprising GPVI is useful for treating
CC   vascular disease, and for reducing platelet activation which involves
CC   contacting platelets with the medicament. The extracellular portion of
CC   GPVI is used therapeutically to attenuate platelet activation and
CC   aggregation and to treat thrombosis and other vascular disorders.
CC   Antibodies generated against GPVI are used as research and
CC   immunotherapeutic agents.
XX
SQ   Sequence  19 AA;

  Query Match                 4.7%;  Score 1.6;  DB 22;  Length 19;
  Best Local Similarity   ...%;  Pred. No. ...e-...;
  Matches  ...;  Conservative  ...;  Mismatches  ...;  Indels  ...;  Gaps  ...;

Qy      61 KESSSKYQLAVLETE 75
           ||||||||||||||| ||
Db       3 KESSSKYQLAVLETE 17


RESULT 29
AAB61272
ID   AAB61272 standard; protein; 57 AA.
XX
AC   AAB61272;
XX
DT   04-APR-2001  (first entry)
XX
DE   Mouse IAN/Pat 268 Ig-like domain #2.
XX
KW   Mouse; IAN/Pat 268; cardiac; cerebroprotective; cytostatic; neuroprotective;
KW   thrombolytic; antibacterial; osteoporosis; Alzheimer's; GPVI;
KW   platelet membrane glycoprotein receptor; bleeding disorder;
KW   blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW   ischaemic cardiovascular disease; immune; viral disease; liver disease;
KW   cancer.
XX
OS   Mus musculus.
```

XX
PN Wo[illegible] AI.
XX
PD [illegible] JAN 2003.
XX
PF [illegible] JUN 2000; 2000WO-US[illegible].
XX
PR [illegible] JUN 1999; [illegible].
PR [illegible] JUN 1999; [illegible].
PR [illegible] FEB 2000; [illegible].
XX
PA (MITS) MITSUBISHI PHARM CORP.
XX
PI [illegible], Yoshida M, Ishii K, Jindra [illegible] M, Yamamoto [illegible] A, [illegible];
PI [illegible] ME, Kinashi T;
XX
DR WPI; 2003-[illegible].
XX
PT New genes encoding human platelet-expressed [illegible];
PT glycoprotein VI, and its modulators, useful in prevention, treatment
PT and diagnosis of hemorrhagic disorders, thrombotic disorders and
PT [illegible] disorders.
XX
PS Disclosure; Page 21-211; 227pp; English.
XX
CC The present sequence is given in a specification describing a novel
CC nucleic acid molecule encoding a platelet membrane glycoprotein
CC glycoprotein VI (GPVI), also called JAND 2/8. The GPVI [illegible]
CC and polypeptides and their modulators, e.g. antibodies [illegible],
CC ribozymes and antibodies, are useful for prevention, treatment and
CC diagnosing disorders associated with aberrant expression [illegible]
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), [illegible]
CC disorders, coronary artery and cerebral artery diseases (e.g. cerebral
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and [illegible]
CC interaction), immunological diseases (e.g. platelet disorders) and
CC embryonic liver disorders. Preferably they are used in prevention
CC cardiac ischaemia following angioplasty and [illegible]
CC especially of the colon and liver.
XX
SQ Sequence 17 AA;

Query Match 4.7%; Score 1.6; DB 22; Length 17;
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches 14; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible] EEIIVIAAHSIYR 47
[illegible]
Db [illegible] EEIIVIAAHSIYR 47

RESULT 3
AAY72798
ID AAY72798 standard; peptide; 17 AA.
XX
AC AAY72798;
XX
DT 31-MAY-2001 (first entry)
XX
DE Human platelet membrane glycoprotein VI (GPVI) peptide 5.
XX
KW Human; platelet membrane glycoprotein VI; GPVI; thrombosis;
KW vascular disease; thrombosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 4
FT /label= Unknown
FT Misc-difference 5
FT /label= Unknown
XX
PN WO200158921-A1.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001WO-US003705.
XX
PR 01-FEB-2000; 2000US-0179447P.
PR 09-FEB-2000; 2000US-0181251P.
XX
PA (SUBA) GLAXO GROUP LTD.
XX
PI Tandon N, Sun B, Nakamura T, Yamamoto N;

PN Wo[illegible]-A1.
XX
PD 08-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-US[illegible].
XX
PR 01-SEP-1999; 1999US-0151[illegible].
PR 09-FEB-2000; 2000US-0181[illegible].
XX
PA (SUBA) GLAXO GROUP LTD.
XX
PI Tandon N, Sun B, Nakamura T, Yamamoto N;
XX
DR WPI; 2001-[illegible].
XX
PT Anti-thrombotic medicament, comprises a polypeptide having the
PT extracellular domain of platelet membrane glycoprotein VI or its
PT variant, useful for treating vascular disease and to treat platelet
PT activation.
XX
PS Claim 1; Page 58; 74pp; English.
XX
CC The present sequence is a human platelet membrane glycoprotein V (GPV)
CC peptide 5, the recitation comprising GPVI is useful for treating
CC vascular disease, and for reducing platelet activation, which occurs
CC contacting platelets with the medicament. The extracellular part of
CC GPVI is used therapeutically to attenuate platelet activation and
CC aggregation and to treat thrombosis and other vascular diseases.
CC Antibodies generated against GPVI are used as research and
CC immunotherapeutic agents.
XX
SQ Sequence 59 AA;

Query Match 4.1%; Score 34; DB 22; Length 59;
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches 14; Conservative [illegible]; Mismatches 0; Indels [illegible]; Gaps [illegible];

Qy 66 RYSDQAVLFIPAMK 79
[illegible]
Db 6 RYSDQAVLFIPAMK 19

RESULT 42
AAY72804
ID AAY72804 standard; peptide; 17 AA.
XX
AC AAY72804;
XX
DT 31-MAY-2001 (first entry)
XX
DE Human platelet membrane glycoprotein VI (GPVI) peptide 1.
XX
KW Human; platelet membrane glycoprotein VI; GPVI; thrombosis;
KW vascular disease; thrombosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 16
FT /label= Unknown
XX
PN WO200158921-A1.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001WO-US003705.
XX
PR 01-FEB-2000; 2000US-0179447P.
PR 09-FEB-2000; 2000US-0181251P.
XX
PA (SUBA) GLAXO GROUP LTD.
XX
PI Tandon N, Sun B, Nakamura T, Yamamoto N;

XX
PN WPI: 2001-228791/24
XX
PT Anti-thrombotic medicament, comprising a polypeptide having the
PT extracellular domain of platelet membrane glycoprotein VI - its
PT variant, useful for treating a vascular disease and reducing platelet
PT activation
XX
PS Disclosure; Page 17; 24pp; English.
XX
CC The present sequence is a human platelet membrane glycoprotein VI (GPVI)
CC peptide 12. The medicament comprising GPVI is used for treating
CC vascular disease and for reducing platelet activation which occurs by
CC contacting platelets with the medicament. The extracellular portion of
CC GPVI is used therapeutically to attenuate platelet activation and
CC aggregation and to treat thrombosis and other vascular diseases.
CC Antibodies generated against GPVI are used as research and
CC immunotherapeutic agents.
XX
SQ Sequence 17 AA;

Query Match 5.3%; Score 12; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 PSRAEPSSLVP 39
|||||||||||
Db 1 PSRAEPSSLVP 12

RESULT 6
AAY72606
ID AAY72606 standard; peptide; 29 AA.
XX
AC AAY72606;
XX
DT 31-MAY-2001 (first entry)
XX
DE Human platelet membrane glycoprotein VI (GPVI) peptide 12.
XX
KW Human; platelet membrane glycoprotein VI; GPVI; thrombolytic therapy;
KW vascular disease; thrombosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 4
FT /note= "Unknown"
FT Misc-difference 7
FT /note= "Unknown"
XX
PN WO200168121-A1.
XX
PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US007976.
XX
PR 14-MAR-2000; 2000US-0525192.
PR 24-MAY-2000; 2000US-0576925.
XX
PA (SUNA) SUNKA PHARM CO LTD.
XX
PI Tatoda N; Sato K; Nakamura I; Yamamoto N;
XX
DR WPI; 2001-628791/24.
XX
PT Anti-thrombotic medicament, comprising a polypeptide having the
PT extracellular domain of platelet membrane glycoprotein VI or its
PT variant, useful for treating a vascular disease and reducing platelet
PT activation
XX
PS Disclosure; Page 17; 24pp; English.
XX
CC The present sequence is a human platelet membrane glycoprotein VI (GPVI)
CC peptide 12. The medicament comprising GPVI is used for treating
CC vascular disease and for reducing platelet activation which occurs by
CC contacting platelets with the medicament. The extracellular portion of
CC GPVI is used therapeutically to attenuate platelet activation and
CC aggregation and to treat thrombosis and other vascular diseases.
CC Antibodies generated against GPVI are used as research and
CC immunotherapeutic agents.
XX
SQ Sequence 29 AA;

Query Match 5.3%; Score 12; DB 22; Length 29;

Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYQLQAVEEIP 11
||||||||||| |
Db 1 SYQLQAVEEIP 11

RESULT 45
AAB41883
ID AAB41883 standard; protein; 265 AA.
XX
AC AAB41883;
XX
DT 11-APR-2000 (first entry)
XX
DE Leukocyte immunoglobulin like receptor LIR-9.
XX
KW Leukocyte immunoglobulin like receptor; LIR; gene therapy;
KW autoimmunity; autoimmune disorder; immune system; drug.
XX
OS Homo sapiens.
XX
PN WO200063383-A2.
XX
PD 26-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US09922.
XX
PR 12-APR-1999; 99US-0128843.
XX
PA (IMMU) IMMUNEX CORP.
XX
PI Cosman D, Anderson DM, Beckmann MP;
XX
DR WPI; 2000-687647/67.
DR N-PSDB; AAA94611.
XX
PT Leukocyte immunoglobulin like receptor (LIR) nucleic acids useful in
PT treating autoimmune diseases and disease states with suppressed immune
PT function.
XX
PS Claim 1; Page 113; 117pp; English.
XX
CC Host cells transformed with a vector which are capable of
CC expressing a leukocyte immunoglobulin like receptor (LIR) can be
CC used to produce the LIR polypeptides. LIR coding sequences are to
CC used in the gene therapy of disorders mediated directly or
CC indirectly by detection of insufficient amounts of any of the LIR
CC polypeptides. The LIR polypeptides can be used to treat autoimmune
CC diseases and disease states with suppressed immune function.
XX
SQ Sequence 265 AA;

Query Match 5.2%; Score 11; DB 21; Length 265;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 294 PSQPELVVPIC 304
||||||||||| |
Db 127 PSQPELVVPIC 137

RESULT 47
AAB04181
ID AAB04181 standard; protein; 275 AA.
XX
AC AAB04181;
XX
DT 11-APR-2000 (first entry)
XX
DE Leukocyte immunoglobulin like receptor LIR-2.
XX
KW Leukocyte immunoglobulin like receptor; LIR; gene therapy;
KW autoimmunity; autoimmune disorder; immune system; drug.
XX
OS Homo sapiens.
XX
PN WO200063383-A2.
XX
PD 26-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US09922.
XX
PR 12-APR-1999; 99US-0128843.
XX
PA (IMMU) IMMUNEX CORP.
XX
PI Cosman D, Anderson DM, Beckmann MP;
XX
DR WPI; 2000-687647/67.

KW Leukocyte immunoglobulin like receptor; LIR; gene therapy;
KW autoimmunity; autoimmune disorder; immune system; drug.
XX
OS Homo sapiens.
XX
PN WO200063383-A2.
XX
PD 26-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US09922.
XX
PR 12-APR-1999; 99US-0128843.
XX
PA (IMMU) IMMUNEX CORP.
XX
PI Cosman D, Anderson DM, Beckmann MP;
XX
DR WPI; 2000-687647/67.

```
RN   [6]
XX
PN   Leukocyte immunoglobulin like receptor (LIR) nucleic acid ...
PN   Treating autoimmune diseases and disease states with suppressed immune
PN   function.
XX
PS   Claim 1; Page 138; 177pp; English.
XX
CC   Host cells transformed with a vector which is capable of
CC   expressing a leukocyte immunoglobulin like receptor (LIR) can be
CC   used to produce the LIR polypeptides. LIR nucleic sequences may be
CC   used in the gene therapy of disorders mediated directly or
CC   indirectly by detective or insufficient amounts of any of the LIR
CC   polypeptides. The LIR polypeptides can be used to treat autoimmune
CC   diseases and disease states with suppressed immune function.
XX
SQ   Sequence  287 AA;

  Query Match          %; Score ; DB ; Length 287;
  Best Local Similarity   %; Pred. No. e-;
  Matches  ; Conservative  ; Mismatches  ; Indels  ; Gaps  ;

Qy      1 MGPGLLVVLT...4
          ||||||||||
Db      1 MGPGLLVVLT...0


RESULT 8
AAW82716
ID   AAW82716 standard; protein; 289 AA.
XX
AC   AAW82716;
XX
DT   20-JUN-2000  (first entry)
XX
DE   Human LIR pbm6.2 protein.
XX
KW   LIR pbm6; immunoregulator; leukocyte immunoglobulin like receptor; LIR;
KW   therapeutic; treatment; disorder; ITIM; MHC class I receptor; inhibitor;
KW   cytoplasmic immunoreceptor tyrosine based inhibitory motif; activator;
KW   neutrophil; basophil; autoimmune disease; suppressed.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FH   -------------------------------------
FT                   /label= signal
FT   Domain          1..201
FT                   /label= extracellular domain
FT   Protein         1..289
FT                   /label= LIR pbm6.2
FT   Domain          202..208
FT                   /label= transmembrane domain
FT   Domain          209..289
FT                   /label= cytoplasmic domain
XX
PN   WO200049017-A1.
XX
PD   24-AUG-2000.
XX
PF   23-APR-2000;   2000WO-US010244.
XX
PR   24-APR-1999;   99US-0131218.
XX
PA   (IMMU ) IMMUNEX CORP.
XX
PI   Dahlen K;
XX
DR   WPI; 2000-570642/51.
DR   N-PSDB; AAW82716.
XX
PT   Leukocyte immunoglobulin like receptor, LIR, polypeptide ... for ...
PT   ... ..., for treating autoimmune diseases or disease states ... with ...
PT   with suppressed immune function.
XX
PS   Claim 4; Page 73; 74pp; English.
XX
CC   This sequence represents a novel leukocyte immunoglobulin like receptor
CC   (LIR) polypeptide LIR-pbm6.2. This sequence can be administered
CC   therapeutically to treat disorders associated with insufficient/deficient
CC   amounts of LIR polypeptides. LIR PRO2 and certain other LIR family members
CC   contain cytoplasmic immunoreceptor tyrosine based inhibitory motif
CC   (ITIMs), whilst other LIR family members lack ITIMs. By analogy with the
CC   structure and function of known MHC class I receptor molecules, LIR
CC   having ITIMs are inhibitory receptors mediating negative stimulation
CC   whilst those lacking ITIMs are activatory receptors. Failure of a
CC   receptor that mediates negative stimulation could result in autoimmune
CC   diseases, whilst failure of a receptor mediating activation, stimulation
CC   could result in suppressed immune function. They are also used to
CC   produce probes for detecting LIR nucleic acids or isolating LIR DNA from
CC   other species.
XX
SQ   Sequence  289 AA;

  Query Match          %; Score ; DB ; Length 289;
  Best Local Similarity   %; Pred. No. e-;
  Matches  ; Conservative  ; Mismatches  ; Indels  ; Gaps  ;

Qy      1 MGPGLLVVLT...4
          ||||||||||
Db      1 MGPGLLVVLT...0


RESULT 9
AAB94173
ID   AAB94173 standard; protein; 289 AA.
XX
AC   AAB94173;
XX
DT   11-APR-2001  (first entry)
XX
DE   Leukocyte immunoglobulin like receptor pbm6.2.
XX
KW   Leukocyte immunoglobulin like receptor; LIR; gene therapy;
KW   autoimmunity; autoimmune disorders; immune system; human; ds
XX
OS   Homo sapiens.
XX
PN   WO200058463-A2.
XX
PD   05-NOV-2000.
XX
PF   12-MAY-2000; 2000WO-US013220.
XX
PR   12-MAY-1999;  99US-0133915.
XX
PA   (IMMU ) IMMUNEX CORP.
XX
PI   Dahlen K; Anderson DM; Bowles D;
XX
DR   WPI; 2000-607643/57.
DR   N-PSDB; AAB94597.
XX
PT   Leukocyte immunoglobulin like receptor (LIR) nucleic acids, useful in
PT   treating autoimmune diseases and disease states with suppressed immune
PT   function.
XX
PS   Example 9; Page 79-80; 177pp; English.
XX
CC   Host cells transformed with a vector which is capable of
CC   expressing a leukocyte immunoglobulin like receptor (LIR), can be
CC   used to produce the LIR polypeptides. LIR nucleic sequences may be
CC   used in the gene therapy of disorders mediated directly or
CC   indirectly by detective or insufficient amounts of any of the LIR
CC   polypeptides. The LIR polypeptides can be used to treat autoimmune
CC   diseases and disease states with suppressed immune function.
```

XX
SQ Sequence 299 AA;

Query Match 4.2%; Score 11; DB 2; Length 299;
Best Local Similarity 15.7%; Pred. No. 1.6e+02;
Matches 11; Conservative 6; Mismatches 3; Indels 2; Gaps 1;

Qy 194 RSEPEEIVVPI 204
:|:|:|:|:|:|:|:|:|:|:
Db 127 RSGEEIVVPI 137

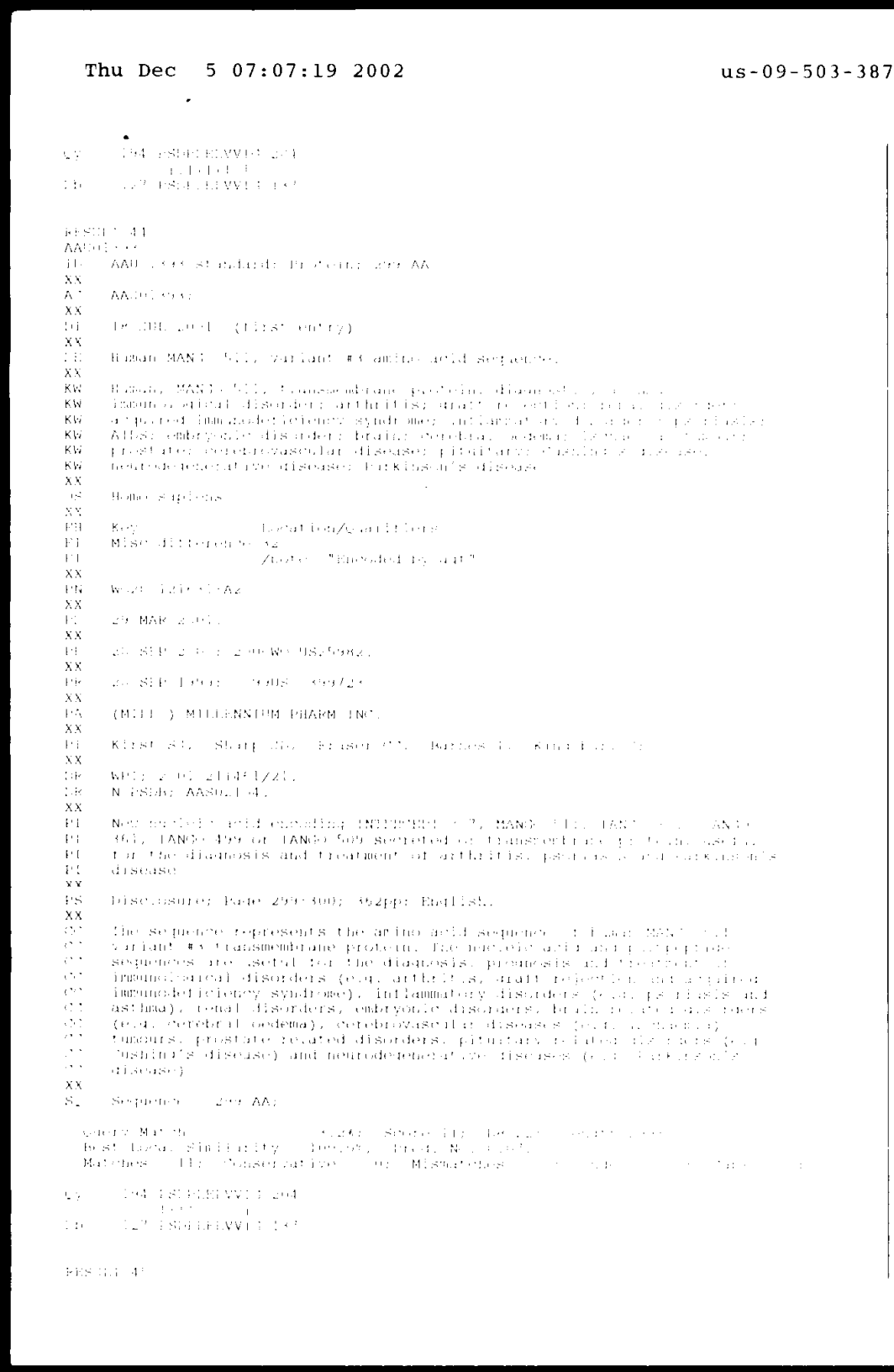
RESULT 11
AAS41196
ID AAS41196 standard; protein; 299 AA.
XX
AC AAS41196;
XX
DT 12-APR-2001 (first entry)
XX
DE Leukocyte immunoglobulin-like receptor LIR-8.
XX
KW Leukocyte immunoglobulin-like receptor; LIR; gene therapy;
KW autoimmunity; anti-immune disorder; immune system disease;
XX
OS Homo sapiens.
XX
PN WO200058466-A2.
XX
PD 5-OCT-2000.
XX
PF 12-MAY-2000; 2000WO-US12828.
XX
PR 12-MAY-1999; 99GB-0011464.
XX
PA (IMMU-) IMMUNEX CORP.
XX
PI Cosman D, Anderson DM, Bovolis E;
XX
DR WPI; 2000-684945/67.
DR N-PSDB; AAS41197.
XX
PT Leukocyte immunoglobulin-like receptor (LIR) polypeptides, nucleic acids
PT encoding them and autoimmune diseases and disease states with which they are
PT implicated.
XX
PS Claim 1; Page 106; 112pp; English.
XX
CC Host cells transformed with a vector which are capable of
CC expressing a leukocyte immunoglobulin-like receptor (LIR) that is
CC used to produce the LIR polypeptides. LIR antibodies polynucleotides
CC used in the gene therapy of disorders mediated directly or
CC indirectly by defective or insufficient amounts of LIR. LIR
CC polypeptides. The LIR polypeptides can be used to treat or detect
CC diseases and disease states with suppressed immune function.
XX
SQ Sequence 299 AA;

Query Match 4.2%; Score 11; DB 2; Length 299;
Best Local Similarity 15.7%; Pred. No. 1.6e+02;
Matches 11; Conservative 6; Mismatches 3; Indels 2; Gaps 1;

Qy 194 RSEPEEIVVPI 204
:|:|:|:|:|:|:|:|:|:|:
Db 127 RSGEEIVVPI 137

RESULT 12
AAS41197
ID AAS41197 standard; protein; 299 AA.
XX
AC AAS41197;
XX
DT 12-APR-2001 (first entry)
XX
DE Human MAN2C 511 amino acid sequence.
XX
KW Human MAN2C 511; transmembrane protein; diagnosis; vaccine;
KW immunological disorder; arthritis; graft rejection; anti-viral; cancer;
KW acquired immunodeficiency syndrome; inflammatory disorder; psoriasis;
KW Alzheimer's disease; brain; cerebral oedema; ischaemic stroke;
KW prostate; cerebrovascular disease; pituitary; pituitary disease;
KW neurodegenerative disease; Parkinson's disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..511
FT /note= "Human peptide"
FT Protein 42..299
FT /note= "Mature MAN2C 511"
FT Domain 42..299
FT /note= "extracellular domain."
FT Modified site 45..45
FT /note= "Asn is N-glycosylated"
FT Modified site 54..54
FT /note= "N myristylation site"
FT Modified site 60..65
FT /note= "N myristylation site"
FT Domain 60..116
FT /note= "Immunoglobulin (Ig) like domain"
FT Modified site 64..67
FT /note= "Protein kinase C phosphorylation site"
FT Modified site 69..74
FT /note= "N myristylation site"
FT Modified site 105..110
FT /note= "Casein kinase II phosphorylation site"
FT Modified site 152..156
FT /note= "Casein kinase II phosphorylation site"
FT Modified site 157..159
FT /note= "Asn is N-glycosylated"
FT Modified site 193..198
FT /note= "N myristylation site"
FT Modified site 207..212
FT /note= "Protein kinase C phosphorylation site"
FT Modified site 217..219
FT /note= "Protein kinase C phosphorylation site"
FT Modified site 238..244
FT /note= "N myristylation site"
FT Modified site 248..253
FT /note= "Asn is N-glycosylated"
FT Domain 266..286
FT /note= "Transmembrane domain"
FT Domain 285..299
FT /note= "Cytoplasmic domain"
FT Modified site 289..294
FT /note= "Protein kinase C phosphorylation site"
XX
PN WO200012683-A2.
XX
PD 20-MAR-2002.
XX
PF 20-SEP-2000; 2000WO-US25908.
XX
PR 20-SEP-1999; 99US-0155725.
XX
PA (MILL-) MILLENNIUM BIOPHARM INC.
XX
PI Kirst HL, Sharp JD, Fraser CC, Barnes D, Kristaponis K;
XX
DR WPI; 2002-211961/21.
DR N-PSDB; AAS41200.
XX
PT Novel nucleic acid encoding a Mitogen-activated protein kinase
PT kinase (MAPKK) or (MAPKK)-associated protein useful
PT for the diagnosis and treatment of arthritis, psoriasis and leukemia.

```
PT   disease
XX
PD   Created: Fri 7: 06pp; English.
XX
CC   The sequence represents the amino acid sequence of human MAN2 ...
CC   transmembrane protein. The nucleic acid and polypeptide sequences
CC   are useful for the diagnosis, prognosis and treatment of immune related
CC   disorders (e.g. arthritis, graft rejection and acquired immunodeficiency
CC   syndrome). Inflammatory disorders (e.g. psoriasis and asthma), renal
CC   disorders, embryonic disorders, brain related disorders (e.g. cerebral
CC   oedema), cerebrovascular diseases (e.g. ischaemia), tumours, prostate
CC   related disorders, pituitary related disorders (e.g. Cushing's disease)
CC   and neurodegenerative diseases (e.g. Parkinson's disease).
XX
SQ   Sequence  ... AA;

  Query Match              %; Score ..; DB ...; Length ...;
  Best Local Similarity    ...%; Pred. No. ...;
  Matches  ..; Conservative  ..; Mismatches  ..; Indels  ..; Gaps  ..;

Qy     ... PSEPLEEVVES ...
           ||||| |||| |
Db     ... PSEPLEEVVES ...


RESULT 12
AAO...
ID   AAO...  standard; Protein; ... AA.
XX
AC   AAO...;
XX
DT   ...-...-2001  (first entry)
XX
DE   Human MAN2 ..., variant #2 amino acid sequence.
XX
KW   Human; MAN2 ...; transmembrane protein; diagnostic; asthma;
KW   immunological disorder; arthritis; graft rejection; renal disorder;
KW   acquired immunodeficiency syndrome; inflammatory disorder; psoriasis;
KW   AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
KW   prostate; cerebrovascular disease; pituitary; Cushing's disease;
KW   neurodegenerative disease; Parkinson's disease.
XX
OS   Homo sapiens.
XX
PN   W...-...-A2.
XX
PD   ... MAR 2...
XX
PF   ... SEP 2...; ...-W-...-2.
XX
PR   ... SEP ...; ...S ...-...-2.
XX
PA   (MILL ) MILLENNIUM PHARM INC.
XX
PI   Kirst HJ, Sharpe BL, Fraser CC, Barnes L, Kiersten S;
XX
DR   WPI; ...-...-Z.
DR   N-PSDB; AAO...
XX
PT   New nucleic acid encoding INTEGRIN-LIKE MAN2 ..., IANP ..., IANP ...
PT   ..., IANP ... or IANP ..., useful for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
PT   disease.
XX
PS   Disclosure; Page ...; ... pp; English.
XX
CC   The sequence represents the amino acid sequence of human MAN2 ...
CC   variant #2 transmembrane protein. The nucleic acid and polypeptide
CC   sequences are useful for the diagnosis, prognosis and treatment of
CC   immunological disorders (e.g. arthritis, graft rejection and acquired
CC   immunodeficiency syndrome). Inflammatory disorders (e.g. psoriasis and
CC   asthma), renal disorders, embryonic disorders, brain related disorders
CC   (e.g. cerebral oedema), cerebrovascular diseases (e.g. ischaemia),
CC   tumours, prostate related disorders, pituitary related disorders (e.g.
CC   Cushing's disease) and neurodegenerative diseases (e.g. Parkinson's
CC   disease).
XX
SQ   Sequence  ... AA;

  Query Match              %; Score ..; DB ...; Length ...;
  Best Local Similarity    ...%; Pred. No. ...;
  Matches  ..; Conservative  ..; Mismatches  ..; Indels  ..; Gaps  ..;

Qy     ... PSEPLEEVVES ...
           ||||| |||| |
Db     ... PSEPLEEVVES ...
```



Qy 194 PSHCEEAVVEG 204
| | | | | | | | | | |
Db 127 PSHLEELVVIG 137

RESULT 44
AAB01694
ID AAB01694 standard; protein; 299 AA.
XX
AC AAB01694;
XX
DT 18-JUL-2001 (first entry)
XX
DE Human MANG 511, variant #4 amino acid sequence.
XX
KW Human; MANG 511; transmembrane protein; diagnostic; antigen;
KW immunological disorder; arthritis; graft rejection; tumour; cancer;
KW acquired immunodeficiency syndrome; inflammatory disorder; psoriasis;
KW AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
KW prostate; cerebrovascular disease; pituitary; Cushing's disease;
KW neurodegenerative disease; Parkinson's disease.
XX
OS Homo sapiens.
XX
PN WO200121651-A2.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000WO-US25992.
XX
PR 23-SEP-1999; 99US-155722P.
XX
PA (MILL) MILLENNIUM PHARM INC.
XX
PI Kirst HI, Sharp JD, Fraser CC, Barnes T, Kinsbury C;
XX
DR WPI; 2001-211461/21.
DR N-PSDB; AAB01694.
XX
PT New nucleic acid encoding INTRINSIC 511, MANG 511, IANG 511, IANG
PT 361, IANG 499 or IANG 509 secreted or transmembrane protein, useful
PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
PT disease
XX
PS Disclosure; Page 299-300; 362pp; English.
XX
CC The sequence represents the amino acid sequence of human MANG 511
CC variant #4 transmembrane protein. The nucleic acid and polypeptide
CC sequences are useful for the diagnosis, prognosis and treatment of
CC immunological disorders (e.g. arthritis, graft rejection and acquired
CC immunodeficiency syndrome), inflammatory disorders (e.g. psoriasis and
CC asthma), renal disorders, embryonic disorders, brain related disorders
CC (e.g. cerebral oedema), cerebrovascular diseases (e.g. ischaemia),
CC tumours, prostate related disorders, pituitary related disorders (e.g.
CC Cushing's disease) and neurodegenerative diseases (e.g. Parkinson's
CC disease).
XX
SQ Sequence 299 AA;

Query Match 1.2%; Score 11; DB 22; Length 299;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 PSHCEEAVVEG 204
| | | | | | | | | | |
Db 127 PSHLEELVVIG 137

RESULT 45
AAB01694
ID AAB01694 standard; protein; 299 AA.
XX
AC AAB01694;
XX
DT 18-JUL-2001 (first entry)
XX
DE Human MANG 511, variant #4 amino acid sequence.
XX
KW Human; MANG 511; transmembrane protein; diagnostic; antigen;
KW immunological disorder; arthritis; graft rejection; tumour; cancer;
KW acquired immunodeficiency syndrome; inflammatory disorder; psoriasis;
KW AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
KW prostate; cerebrovascular disease; pituitary; Cushing's disease;
KW neurodegenerative disease; Parkinson's disease.
XX
OS Homo sapiens.
XX
PN WO200121651-A2.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000WO-US25992.
XX
PR 23-SEP-1999; 99US-155722P.
XX
PA (MILL) MILLENNIUM PHARM INC.
XX
PI Kirst HI, Sharp JD, Fraser CC, Barnes T, Kinsbury C;
XX
DR WPI; 2001-211461/21.
DR N-PSDB; AAB01694.
XX
PT New nucleic acid encoding INTRINSIC 507, MANG 511, IANG 511, IANG
PT 361, IANG 499 or IANG 509 secreted or transmembrane protein, useful
PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
PT disease
XX
PS Disclosure; Page 301-302; 362pp; English.
XX
CC The sequence represents the amino acid sequence of human MANG 511
CC variant #4 transmembrane protein. The nucleic acid and polypeptide
CC sequences are useful for the diagnosis, prognosis and treatment of
CC immunological disorders (e.g. arthritis, graft rejection and acquired
CC immunodeficiency syndrome), inflammatory disorders (e.g. psoriasis and
CC asthma), renal disorders, embryonic disorders, brain related disorders
CC (e.g. cerebral oedema), cerebrovascular diseases (e.g. ischaemia),
CC tumours, prostate related disorders, pituitary related disorders (e.g.
CC Cushing's disease) and neurodegenerative diseases (e.g. Parkinson's
CC disease).
XX
SQ Sequence 299 AA;

Query Match 1.2%; Score 11; DB 22; Length 299;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 PSHCEEAVVEG 204
| | | | | | | | | | |
Db 127 PSHLEELVVIG 137

RESULT 46
AAB16362
ID AAB16362 standard; protein; 47 AA.
XX
AC AAB16362;
XX
DT 28-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #16362.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; prognosis;

```
KW   Soluble cytokine receptor; leukemia; immune disorder; cytokine; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001
XX
PF   05-MAR-2001; 2001WO-US006941.
XX
PR   05-MAR-2000; 2000US-186727P.
PR   13-APR-2000; 2000US-196472P.
XX
PA   (HYSE ) HYSEQ INC.
XX
PI   Drmanac RD, Drmanac SD, Jones VJ;
XX
DR   WPI; 2001-664972/76.
DR   N-PSDB; AAV67414.
XX
PT   New isolated polynucleotide and encoded polypeptide, useful in
PT   diagnosis, forensics, gene mapping, identification, treating
PT   susceptibility to genetic disorders or other traits and in assays
PT   for effectors
XX
PS   Claim 20; SEQ ID NO 46743; 1 Spp; English.
XX
CC   The invention relates to isolated polynucleotide (I), and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   in expression analysis, restriction (RFLP) primers, chromosome and
CC   gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy, methods
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, identifying
CC   specific binding partners, any molecule which binds to it, detecting it
CC   quantitatively in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical
CC   treatment of diseases associated with (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of variations
CC   responsible for genetic disorders or other traits, to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. Abs0001Q-Abs0477 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from
CC   http://ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   57 AA;

  Query Match             5.2%;  Score 11;  DB 22;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      194 PSDFLELVVIG 204
            ||||||||||| |
Db      298 PSDFLELVVIG 288


RESULT 17
AAW82940
ID   AAW82940 standard; Protein; 189 AA.
XX
AC   AAW82940;
XX
DT   ??-FEB-2002  (first entry)
XX
DE   Human ITB phase 4 protein.
XX
KW   Integrin; immunoregulation; leukocyte migration; cell adhesion; cell signalling;
KW   therapeutic; treatment; disorder; ITIM; MHC class I receptor; inhibitory;
KW   cytoplasmic immunoreceptor tyrosine based inhibitory motif; ITB; cytokine;
KW   cytokine signalling; immunodeficiency; autoimmune disease; suppressor; ITP
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Propeptide      1..19
FT                   /label= signal
FT   Domain          1..401
FT                   /label= extracellular domain
FT   Protein         17..189
FT                   /label= ITB phase 4
FT   Domain          402..406
FT                   /label= transmembrane region
FT   Domain          407..459
FT                   /label= cytoplasmic domain
XX
PN   WO200249917-A1.
XX
PD   27-JUN-2002.
XX
PF   21-DEC-2001;   2001WO-US050243.
XX
PR   24-APR-2001;   2001US-0841218.
XX
PA   (IMMU ) IMMUNEX CORP.
XX
PI   Dickinson EO;
XX
DR   WPI; 2002-608009/65.
DR   N-PSDB; AAV63455.
XX
PT   Leukocyte immunoglobulin like receptor, LIR, polypeptides useful
PT   for treating autoimmune diseases or disease states associated
PT   with suppressed immune function
XX
PS   Claim 4; Page 77; 78pp; English.
XX
CC   This sequence represents a novel leukocyte immunoglobulin like receptor
CC   (LIR) polypeptide LIR pmb86.4. This sequence can be administered
CC   therapeutically to treat disorders associated with insufficient/defective
CC   amounts of LIR polypeptide. LIR PB02 and certain other LIR family members
CC   contain cytoplasmic immunoreceptor tyrosine based inhibitory motifs
CC   (ITIMs), whilst other LIR family members lack ITIMs. By analogy with the
CC   structure and function of known MHC class I receptors in humans, LIRs
CC   having ITIMs are inhibitory receptors mediating negative signalling,
CC   whilst those lacking ITIMs are activatory receptors, ligation of a
CC   receptor that mediates negative signal, the overall result is an immune
CC   response, whilst failure of a receptor mediating activatory signalling
CC   could result in suppressed immune function. They are also useful to
CC   produce probes for detecting LIR nucleic acids or isolating LIR DNA from
CC   other species.
XX
SQ   Sequence   489 AA;

  Query Match             4.2%;  Score 11;  DB 18;  Length 489;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      194 PSDFLELVVIG 204
            ||||||||||| |
Db      120 PSDFLELVVIG 130


RESULT 58
AAP94171
ID   AAP94171 standard; Protein; 459 AA.
XX
AC   AAP94171;
XX
DT   11-APR-2002  (first entry)
XX
DE   Leukocyte immunoglobulin like receptor 4 plus 6.
XX
```

KW Leukocyte immunoglobulin like receptor; LIR; gene therapy;
KW rheumatoid arthritis; autoimmune disease; immune system disorder.
XX
OS Homo sapiens.
XX
PN WO200068383-A2.
XX
PD 16-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-US12928.
XX
PR 12-MAY-1999; 99US-0134063.
XX
PA (IMMU) IMMUNEX CORP.
XX
PI Beckmann MP, Anderson DM, Fanslow WC;
XX
DR WPI; 2000-654067/62.
DR N-PSDB; AAA54908.
XX
PT Leukocyte immunoglobulin like receptor (LIR) nucleic acid, for
PT treating autoimmune diseases and disease states with suppressed immune
PT function
XX
PS Example 6; Page 85; 117pp; English.
XX
CC Host cells transformed with a vector which can express a
CC expressing a leukocyte immunoglobulin like receptor (LIR) which is
CC used to produce the LIR polypeptides. LIR-coding sequences are also
CC used in the gene therapy of disorders mediated directly or
CC indirectly by detective or insufficient amounts of LIR. The LIR
CC polypeptides. The LIR polypeptides can be used to treat autoimmune
CC diseases and disease states with suppressed immune function
XX
SQ Sequence 488 AA;

Query Match 5.7%; Score 11; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 PSPPEIVVG 204
||||||||| |
Db 110 PSPPEIVVG 120

RESULT 19
ABG10567
ID ABG10567 standard; protein; 177 AA.
XX
AC ABG10567;
XX
DT 28-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #10148.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10641.
XX
PR 31-MAR-2000; 2000US-0540017.
PR 28-AUG-2000; 2000US-0649167.
XX
PA (HYSE) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-650962/73.
DR N-PSDB; AAS74344.
XX
PT New isolated protein- and extended polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of traits
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 20; SEQ ID NO 4; 72pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers and in chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy methods
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, as vaccines,
CC pharmaceutical agents, in tissue engineering protocols and as a food
CC supplement. (II) and its binding partners are useful in methods
CC identification of sites expressed (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of traits
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AB6568 - AB6585377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: the sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 177 AA;

Query Match 5.7%; Score 11; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 KPSLSAQDSP 124
||||||||||
Db 75 KPSLSAQDSP 84

RESULT 5
ABG10563
ID ABG10563 standard; protein; 350 AA.
XX
AC ABG10563;
XX
DT 14-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #10154.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10636.
XX
PR 31-MAR-2000; 2000US-0540017.
PR 28-AUG-2000; 2000US-0649167.
XX
PA (HYSE) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-650962/73.
DR N-PSDB; AAS74350.

```
XX
PT   New isolated polynucleotide and encoded polypeptides useful in
PT   diagnostics, forensics, gene mapping, identification of genes
PT   responsible for genetic disorders or other traits and to
PT   medicinals
XX
PN   WO200246455-A2.
XX
PD   13-JUN-2002; 2002WO-US038622 (06-DEC-2002).
XX
PR   06-DEC-2001; 2001US-0337000P.
XX
PA   Incyte Genomics, Inc.
XX
PI   The invention relates to isolated polynucleotide (I) and
PI   polypeptide (II) sequences. (I) is useful as hybridisation probes,
PI   polymerase chain reaction (PCR) primers, oligomers, and in recombinant
PI   and gene mapping, and in recombinant production of (II). The
PI   polynucleotides are also used in diagnostics as expression profiles and
PI   for identifying expressed genes. (I) is useful in gene therapy techniques
PI   to restore normal activity of (II) or to treat disease states in which
PI   (II). (I) is useful for generating antibodies against it, detecting or
PI   quantitating a polypeptide in tissue, as molecular weight markers and as
PI   a food supplement. (II) and its binding partners are also useful in detecting
PI   binding of sites expressing (II). (I) and (II) are useful for treating
PI   disorders including aberrant protein expression or activity.
PI   The polypeptide and polynucleotide sequences have applications in
PI   diagnostics, forensics, gene mapping, identification of genes
PI   responsible for genetic disorders or other traits to assess biological
PI   and to produce other types of data and products dependent on DNA and
PI   amino acid sequences. AB(Gastrin-Ab(2)s27 represents novel human
PI   diagnostic amino acid sequences of the invention.
PI   Note: The sequence data for this patent did not appear in the printed
PI   specification, but was obtained in electronic format directly from WIPO
PI   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence  378 AA;

  Query Match             2.9%;  Score 13;  DB 22;  Length 378;
  Best Local Similarity   50.0%;  Pred. No. 2.1;
  Matches    7;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      13 KLSISAVDSE 22
           |||||||||
Db     114 KLSISAVDLE 123


Search completed: December 6, 2002, 06:57:25
Job time : 41 secs
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GM protein - protein search, using sw model

Run on: December 5, 2002, 07:07:23 ; Search time 1.5 Seconds
(without alignments)
1011.983 Million cell updates/sec

Title: US-09-503-387-3

Perfect score: 1286

Sequence: 1 MSPSPIALPCQAQGRVPA.....KSPPSQ 196

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 28224 seqs, 9634122 residues

Total number of hits satisfying chosen parameters: 28224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

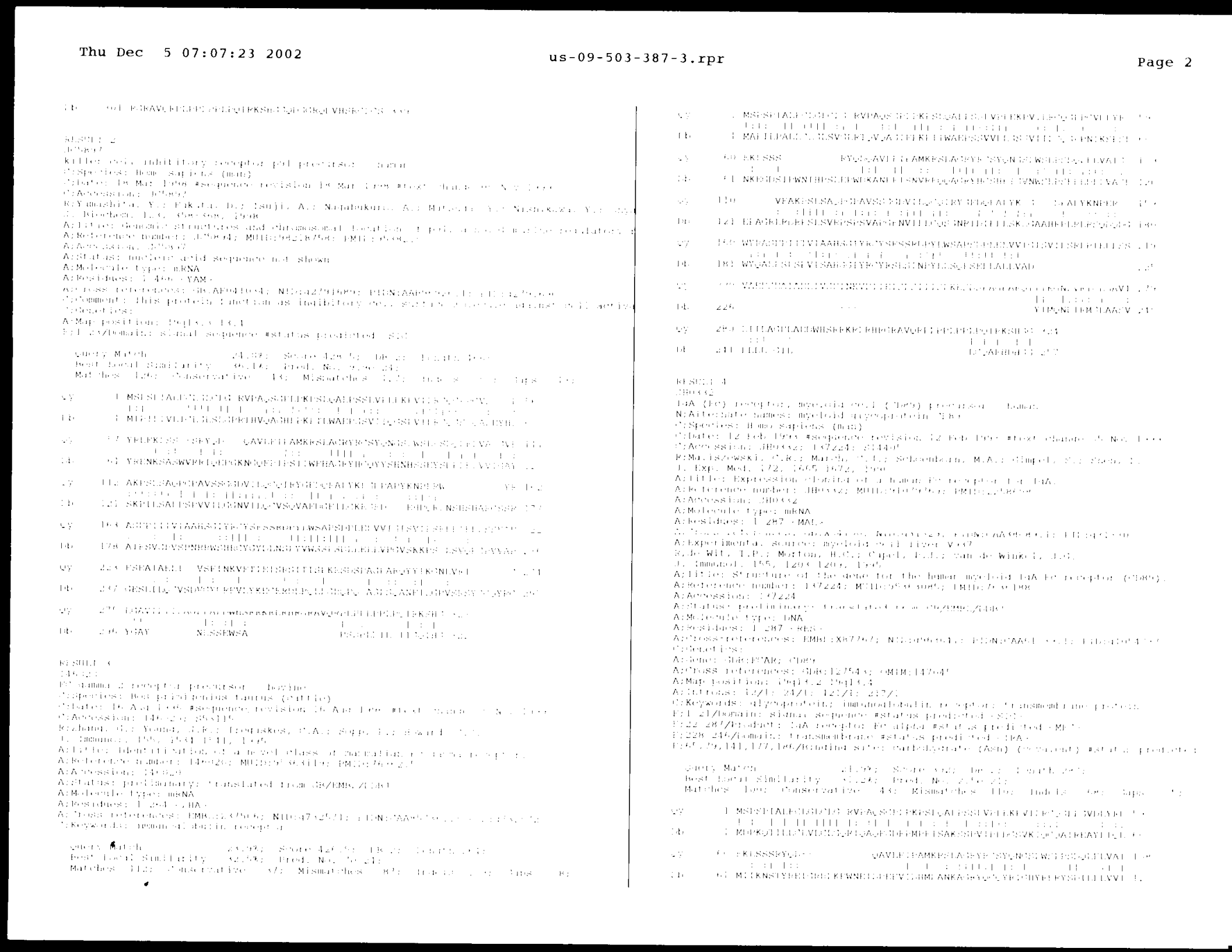
SUMMARIES

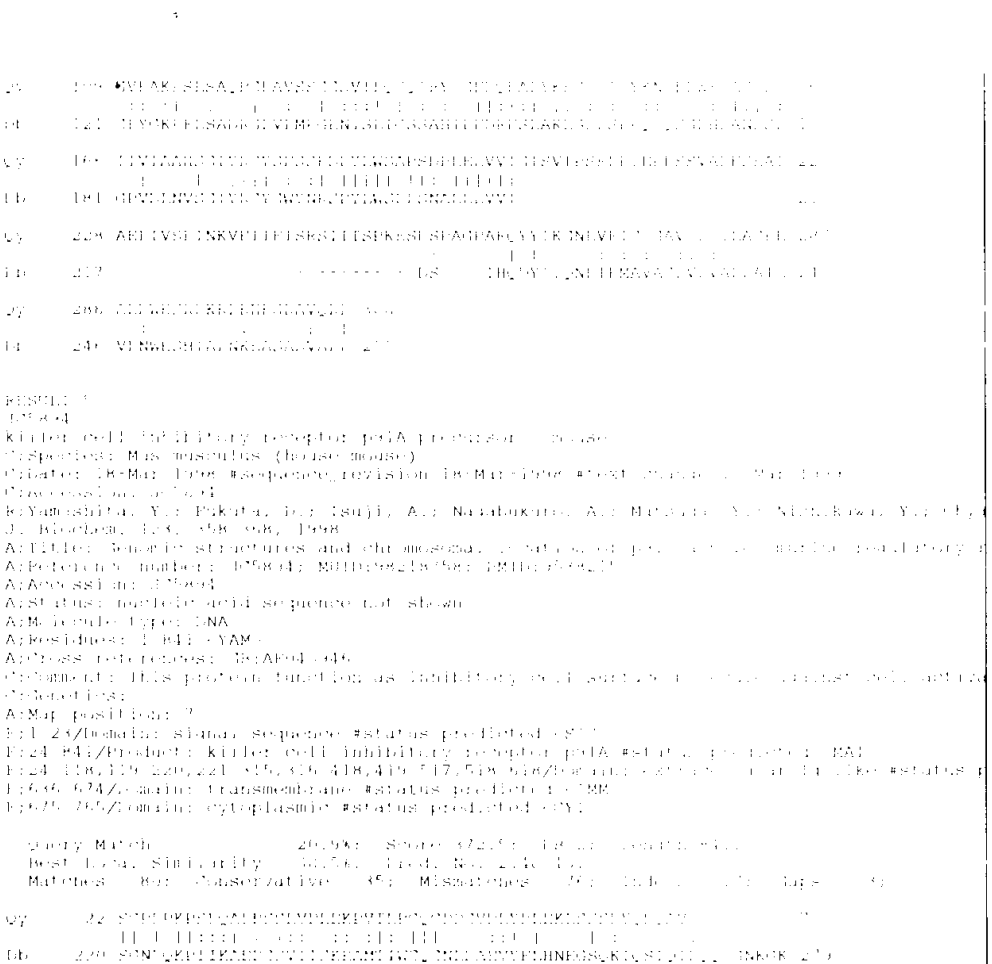
Result No.	Score	Query Match	Length	DB	ID	Description
1	1286	100	330	2	A55092	alpha-2-macroglo
2	428.5	24.9	466	2	I59092	alpha-2-macroglo
3	426.5	24.9	264	2	I46021	T-cell receptor
4	392	21.9	287	2	JH0332	HLA-DRB beta pol
5	372.5	21.9	811	2	JT5891	alpha-2-macroglo
6	369.5	20.5	665	2	JT5896	alpha-2-macroglo
7	358.5	20.1	259	2	G02690	T-cell receptor
8	344	19.3	411	2	S09625	----------- ----
9	337	19.8	414	2	S01925	Ig kappa (fragm
10	330	18.5	246	2	I57434	T-cell receptor
11	328	18.4	438	2	A57247	alpha-2-macroglo
12	327	18.3	447	2	S01924	Ig kappa (fragm
13	323.5	18.1	411	2	I01725	serine-type pro
14	322	18.0	1327	2	T09402	Tumor-specific
15	317.5	17.8	435	2	A54434	T-cell receptor
16	316	17.7	455	2	G01928	Ig kappa (fragm
17	315	17.6	427	2	G02054	Ig kappa (fragm
18	299.5	16.8	501	2	A41857	proteinase inhi
19	292	16.3	184	2	I46455	T-cell receptor
20	145	8.1	265	2	A42547	Ig heavy chain
21	132.5	8.0	474	1	CMMSIB	alpha-1-B glyco
22	129.5	7.1	4787	2	S20855	fibrinogen alph
23	124.5	7.0	262	2	I56116	T-cell receptor
24	124.5	6.9	267	2	A45992	T-cell receptor
25	116	6.5	4492	2	A48066	protein-tyrosin
26	116	6.5	2774	2	A45459	Ig heavy chain
27	115	6.4	283	1	EQMSSI	T-cell receptor
28	113.5	6.3	1256	2	A43425	protein YAM - m
29	113.5	6.3	592	2	I70864	T-cell receptor
30	113.5	6.3	1256	2	A53840	Source: Yeti ad
31	111.5	6.2	1012	2	I45865	60S ribosomal p
32	111	6.2	267	2	A41656	Ig heavy chain
33	109.5	6.1	410	2	I42433	T-cell receptor
34	108	6.0	257	2	S50382	IgE Fc receptor
35	107	6.0	281	2	S21500	Ig kappa (fragm
36	106.5	6.0	4571	2	I10821	type VI collage
37	106	5.9	247	2	S50903	Ig kappa (fragm
38	105	5.9	1256	2	JN0582	Substrate adhes
39	105	5.9	99	2	I47710	Interferon alph
4	105	5.9	270	2	I42857	Ig kappa chain
40	105.5	5.9	99	2	A43771	Ig kappa (fragm
41	105.5	5.9	99	2	I47966	Ig kappa chain
42	105.5	5.9	99	2	I47967	Ig kappa chain
43	104.5	5.9	247	2	I47982	Ig kappa chain
44	104.5	5.9	105	2	I11168	Transmembrane g
45	104	5.8	270	2	S43476	Ig kappa chain

ALIGNMENTS

RESULT 1
P07996
glycoprotein VI I - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2002
C;Accession: P07996; P07716
R;Erickson, H.P.; Ochiyama, T.; Takayama, H.
Biochem. Biophys. Res. Commun. 277, 27-36, 2000
A;Title: Molecular electron density structure, shape, intermediates, and oligomer
A;Reference number: P07996; MUID:21036674; PMID:11027644
A;Contents: Protein
A;Accession: P07996
A;Molecule type: mRNA
A;Residues: 1-330; E27-
A;Cross-references: DDBJ:AB044810
A;Accession: P07101
A;Molecule type: protein
A;Residues: 28-41;62-72;113-142;222-
C;Comment: This protein, which belongs to the immunoglobulin superfamily, is the major component of platelet membrane glycoprotein IV (GP IV), and plays a role in collagen binding.
C;Genetics:
A;Gene: gpVI I
A;Map position: 19q13.4
A;Introns: 27/1; 95/2; 141/3; 193/1; 232/1; 277/2
C;Keywords: glycoprotein; immunoglobulin; platelet

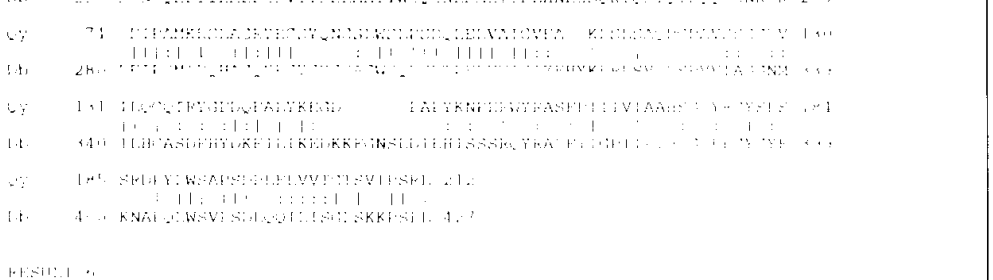
Query Match 100.0%; Score 1286; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.2e-122;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





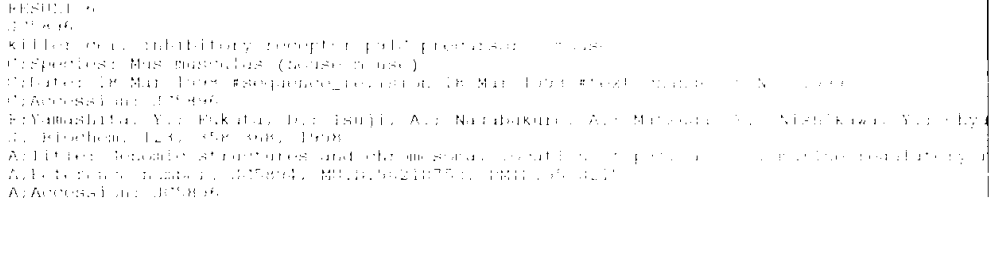
RESULT 5
D75964
killer cell inhibitory receptor p49A precursor - mouse
O;Species: Mus musculus (house mouse)
O;Date: 28-Mar-1998 #sequence_revision 28-Mar-1998 #text_change 09-Jul-1999
O;Accession: D75964
R;Yamashita, Y.; Fukata, Y.; Isuji, A.; Nanabokuro, A.; Miyata, Y.; Nishikawa, Y.; Ly
J. Biochem. 123, 458-468, 1998
A;Title: Genomic structures and chromosomal localization of paired killer inhibitory
A;Reference number: D75964; MUID:98210775; PMID:9504427
A;Accession: D75964
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-841 <YAM>
A;Cross-references: GB:AF041446
C;Comment: This protein functions as inhibitory cell surface receptor which negativ
C;Genetics:
A;Map position: 7
F;1-24/Domain: signal sequence #status predicted <SIG>
F;24-841/Product: killer cell inhibitory receptor p49A #status predicted <MAT>
F;24-138,179-220,241-315,336-418,439-517/Domain: extracellular #status predicted
F;636-674/Domain: transmembrane #status predicted <TRM>
F;675-765/Domain: cytoplasmic #status predicted <CYT>

Query Match 26.9%; Score 474.5; DB 2; Length 841;
Best Local Similarity 56.5%; Pred. No. 2.6e-17;
Matches 84; Conservative 45; Mismatches 37; Indels 3; Gaps 1;



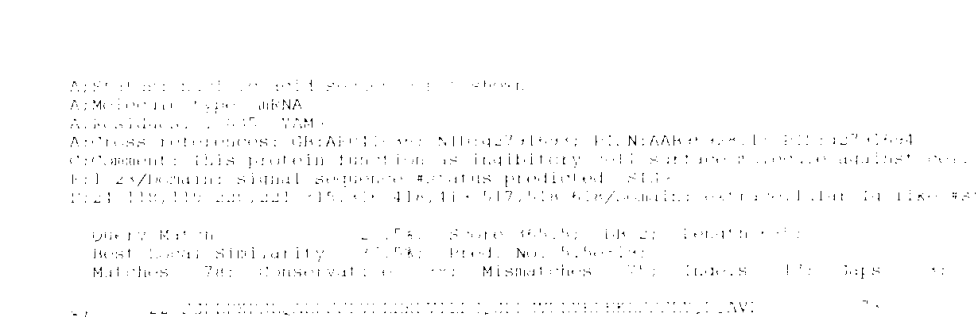
RESULT 6
D75965
killer cell inhibitory receptor p49B precursor - mouse
O;Species: Mus musculus (house mouse)
O;Date: 28-Mar-1998 #sequence_revision 28-Mar-1998 #text_change 09-Jul-1999
O;Accession: D75965
R;Yamashita, Y.; Fukata, Y.; Isuji, A.; Nanabokuro, A.; Miyata, Y.; Nishikawa, Y.; Ly
J. Biochem. 123, 458-468, 1998
A;Title: Genomic structures and chromosomal localization of paired killer inhibitory
A;Reference number: D75964; MUID:98210775; PMID:9504427
A;Accession: D75965
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-841 <YAM>
A;Cross-references: GB:AF041447
C;Comments: This protein functions as inhibitory cell surface receptor which negativ
C;Genetics:
A;Map position: 7
F;1-24/Domain: signal sequence #status predicted <SIG>
F;24-841/Product: killer cell inhibitory receptor p49B #status predicted <MAT>
F;24-138,179-220,241-315,336-418,439-517/Domain: extracellular #status predicted
F;636-674/Domain: transmembrane #status predicted <TRM>
F;675-765/Domain: cytoplasmic #status predicted <CYT>

Query Match 26.9%; Score 474.5; DB 2; Length 841;
Best Local Similarity 56.5%; Pred. No. 2.6e-17;
Matches 84; Conservative 45; Mismatches 37; Indels 3; Gaps 1;

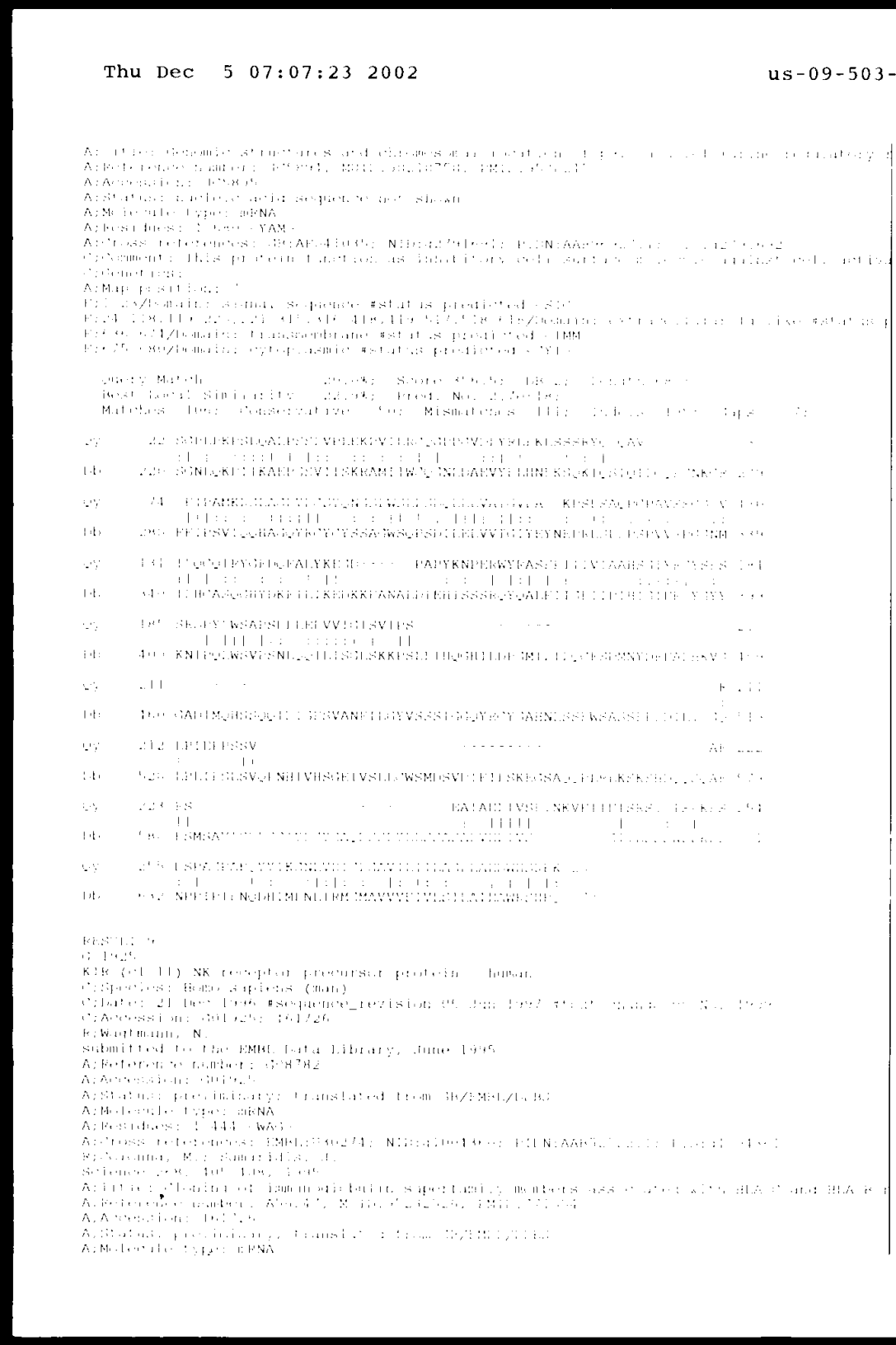


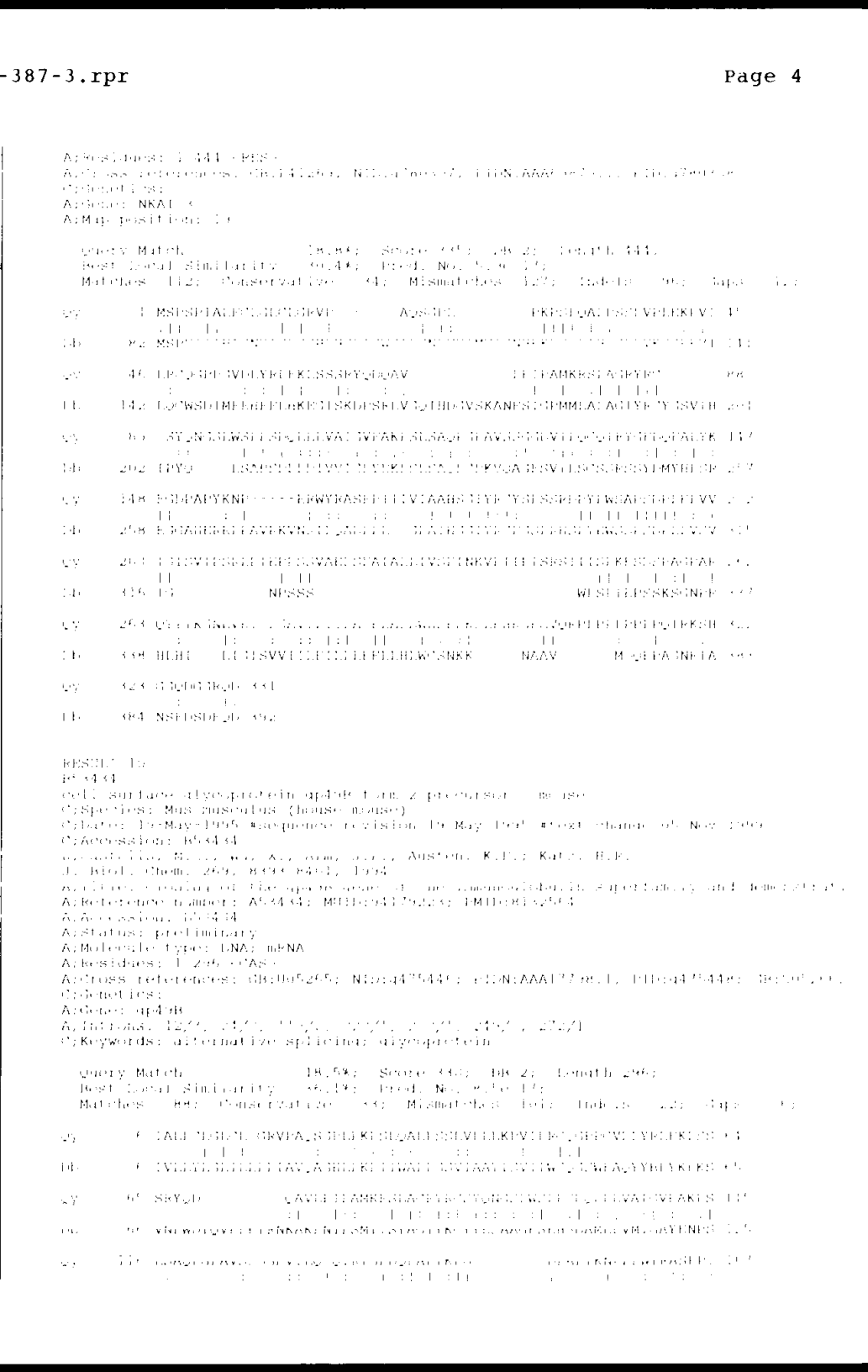
RESULT 7
G02650
Fc alpha/mu receptor - human
O;Species: Homo sapiens (man)
O;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 27-Jul-1999
O;Accession: G02650
Kerr, J.R.; Morton, H.C.; Matthijnssen, E.; Brunke, M.; Bakkers, J.A.M.; Jac
Submitted to the EMBL Data Library, April 1996
R;Reference number: H01508
A;Accession: G02650
A;Status: preliminary; translated from GB/EMBL/Bank
A;Molecule type: mRNA
A;Residues: 1-239 <VAN>
A;Cross-references: EMBL:Z77...; NID:g1320228; PID:g1320229

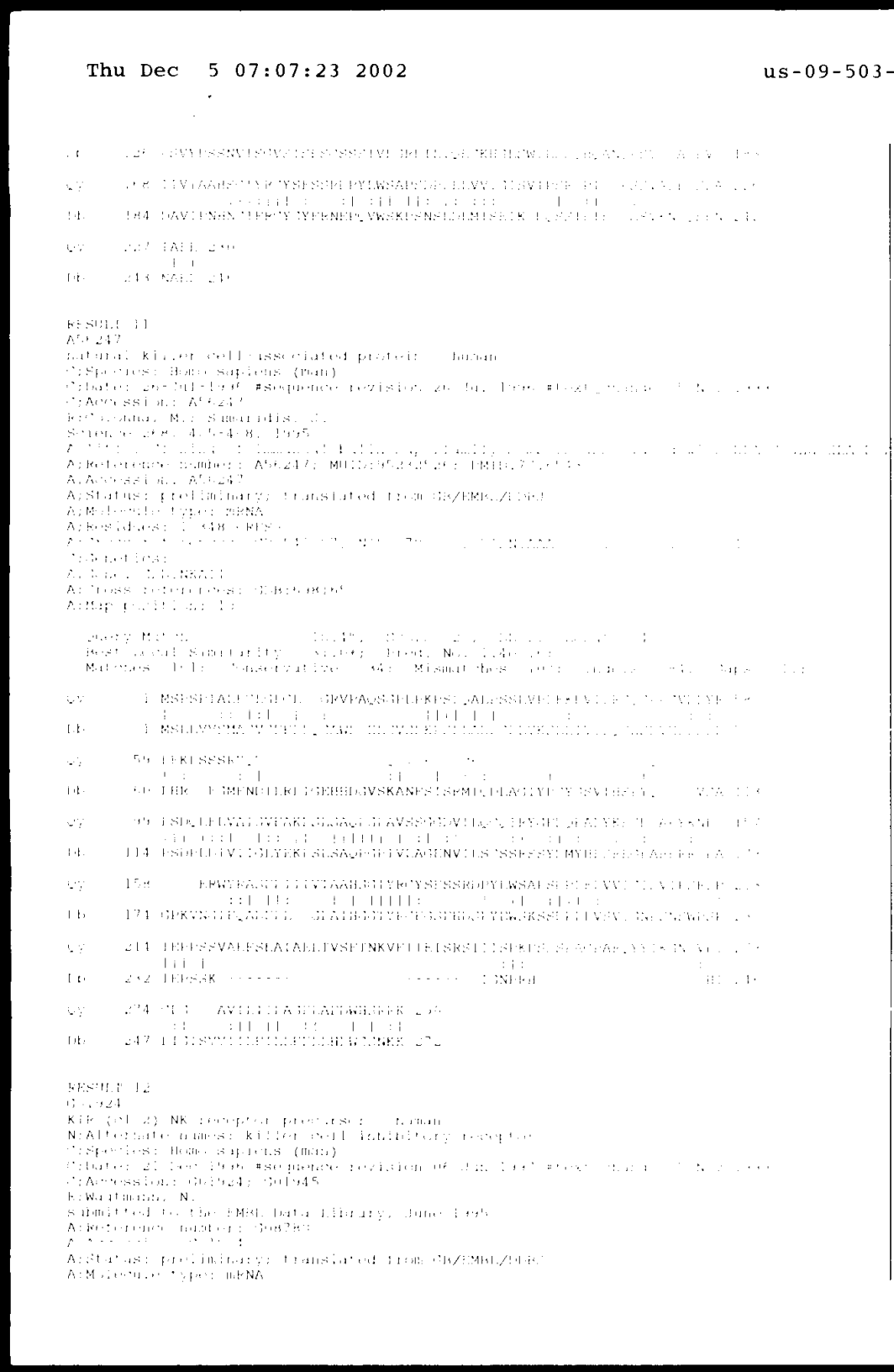
Query Match 23.1%; Score 358.5; DB 2; Length 239;
Best Local Similarity 56.7%; Pred. No. 5.5e-14;
Matches 84; Conservative 45; Mismatches 35; Indels 3; Gaps 1;



RESULT 8
D75965
killer cell inhibitory receptor p49B precursor - mouse
O;Species: Mus musculus (house mouse)
O;Date: 28-Mar-1998 #sequence_revision 28-Mar-1998 #text_change 09-Nov-1999
O;Accession: D75965
R;Yamashita, Y.; Fukata, Y.; Isuji, A.; Nanabokuro, A.; Miyata, Y.; Nishikawa, Y.;
J. Biochem. 123, 458-468, 1998







RESULT 11
A56247
natural killer cell-associated protein - human
C;Species: Homo sapiens (man)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-1999
C;Accession: A56247
R;Colonna, M.; Samaridis, J.
Science 268, 405-408, 1995
A;Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B recognition by human natural killer cells.
A;Reference number: A56247; MUID:95262525; PMID:7716543
A;Accession: A56247
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-438 <KES>
A;Cross-references: GB:U24183; NID:g1008104; PIDN:AAA60401.1; PID:g1008105
C;Genetics:
A;Gene: NKAT2

Query Match 99.8%; Score 2211; DB 2; Length 444;
Best Local Similarity 99.1%; Pred. No. 2.3e-191;
Matches 441; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSESPEALPSLGCVLVPVLLAGPRPAEGPRPSFWAMESQETEASVVLKCVKVSDFQPPSMI 60

Db 1 MSESPEALPSLGCVLVPVLLAGPRPAEGPRPSFWAMESQETEASVVLKCVKVSDFQPPSMI 60

Qy 61 EWYKNNKKIEQEKGIRVDIKDKYIHQKSLFYLRIVHLTEKDEGIYNCIGIIVGLEDTVQI 120

Db 61 EWYKNNKKIEQEKGIRVDIKDKYIHQKSLFYLRIVHLTEKDEGIYNCIGIIVGLEDTVQI 120

Qy 121 DLTVHSKPKITSFDSPTNVNEGKEVNLTCDAESKPEPTVSWWKDGVQLKKDNTLSLRHVT 180

Db 121 DLTVHSKPKITSFDSPTNVNEGKEVNLTCDAESKPEPTVSWWKDGVQLKKDNTLSLRHVT 180

Qy 181 RKHSGTYTCQGSHLYTELSSVVSLFVPVSQGASTTPAVHMDSDHLTILIFVTVVIILTLF 240

Db 181 RKHSGTYTCQGSHLYTELSSVVSLFVPVSQGASTTPAVHMDSDHLTILIFVTVVIILTLF 240

Qy 241 VLWIYKHRNRDRTIDESKRVDYDIHVNYSPAYSDPLQKSTRLSTDVMNMEAGNSSQPNSS 300

Db 241 VLWIYKHRNRDRTIDESKRVDYDIHVNYSPAYSDPLQKSTRLSTDVMNMEAGNSSQPNSS 300

Qy 301 DTGEEDIGETSYYCNQSVEGGIGNSTSTGRIIHGDSVLGLQPLAGNVKDPTLVSGSMDGP 360

Db 301 DTGEEDIGETSYYCNQSVEGGIGNSTSTGRIIHGDSVLGLQPLAGNVKDPTLVSGSMDGP 360

Qy 361 RAPHLSLSPKSHLEIPTLSSSPQKSSPSLLSSTESKESSALYLGQLQTLRIADTALYICVP 420

Db 361 RAPHLSLSPKSHLEIPTLSSSPQKSSPSLLSSTESKESSALYLGQLQTLRIADTALYICVP 420

Qy 421 RSRAPSLRSITV 432

Db 421 RSRAPSLRSITV 432

RESULT 12
U24183
NKR (pl 2) NK receptor precursor - human
N;Alternate names: killer cell inhibitory receptor
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1995 #sequence_revision 08-Jan-1997 #text_change 09-Jul-1999
C;Accession: U24183; S01945
R;Wagtmann, N.
Submitted to the EMBL Data Library, June 1995
A;Reference number: S01945
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-444 <WAG>
A;Cross-references: EMBL:U24183; NID:g1008104; PIDN:AAA60401.1; PID:g1008105
R;Valiante, N.M.; Phillips, J.H.; Lanier, L.L.; Parham, P.
J. Immunol. 157, 1418-1427, 1996
A;Title: Killer cell receptor-ligand interactions: human NK cells and single-chain class I MHC molecules.
A;Reference number: A56245; MUID:96387124; PMID:8759731
A;Accession: A56245
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-438 <VAL>
A;Cross-references: GB:U24183; NID:g1008104; PIDN:AAA60401.1; PID:g1008105
C;Genetics:
A;Gene: NKAT2

Query Match 99.8%; Score 2211; DB 2; Length 444;
Best Local Similarity 99.1%; Pred. No. 2.3e-191;
Matches 441; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSESPEALPSLGCVLVPVLLAGPRPAEGPRPSFWAMESQETEASVVLKCVKVSDFQPPSMI 60

Db 1 MSESPEALPSLGCVLVPVLLAGPRPAEGPRPSFWAMESQETEASVVLKCVKVSDFQPPSMI 60

Qy 61 EWYKNNKKIEQEKGIRVDIKDKYIHQKSLFYLRIVHLTEKDEGIYNCIGIIVGLEDTVQI 120

Db 61 EWYKNNKKIEQEKGIRVDIKDKYIHQKSLFYLRIVHLTEKDEGIYNCIGIIVGLEDTVQI 120

Qy 121 DLTVHSKPKITSFDSPTNVNEGKEVNLTCDAESKPEPTVSWWKDGVQLKKDNTLSLRHVT 180

Db 121 DLTVHSKPKITSFDSPTNVNEGKEVNLTCDAESKPEPTVSWWKDGVQLKKDNTLSLRHVT 180

Qy 181 RKHSGTYTCQGSHLYTELSSVVSLFVPVSQGASTTPAVHMDSDHLTILIFVTVVIILTLF 240

Db 181 RKHSGTYTCQGSHLYTELSSVVSLFVPVSQGASTTPAVHMDSDHLTILIFVTVVIILTLF 240

Qy 241 VLWIYKHRNRDRTIDESKRVDYDIHVNYSPAYSDPLQKSTRLSTDVMNMEAGNSSQPNSS 300

Db 241 VLWIYKHRNRDRTIDESKRVDYDIHVNYSPAYSDPLQKSTRLSTDVMNMEAGNSSQPNSS 300

Qy 301 DTGEEDIGETSYYCNQSVEGGIGNSTSTGRIIHGDSVLGLQPLAGNVKDPTLVSGSMDGP 360

Db 301 DTGEEDIGETSYYCNQSVEGGIGNSTSTGRIIHGDSVLGLQPLAGNVKDPTLVSGSMDGP 360

Qy 361 RAPHLSLSPKSHLEIPTLSSSPQKSSPSLLSSTESKESSALYLGQLQTLRIADTALYICVP 420

Db 361 RAPHLSLSPKSHLEIPTLSSSPQKSSPSLLSSTESKESSALYLGQLQTLRIADTALYICVP 420

Qy 421 RSRAPSLRSITV 432

Db 421 RSRAPSLRSITV 432

RESULT 13
I61725
natural killer associated transcript 2 - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-1999
C;Accession: I61725
R;Colonna, M.; Samaridis, J.
Science 268, 405-408, 1995
A;Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B recognition by human natural killer cells.
A;Reference number: A56247; MUID:95262526; PMID:7716543
A;Accession: I61725
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-441 <KES>
A;Cross-references: GB:U24182; NID:g1008103; PIDN:AAA60400.1; PID:g1008104
C;Genetics:
A;Gene: NKAT-2

Query Match 99.8%; Score 2211; DB 2; Length 441;
Best Local Similarity 99.1%; Pred. No. 2.3e-191;
Matches 441; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSESPEALPSLGCVLVPVLLAGPRPAEGPRPSFWAMESQETEASVVLKCVKVSDFQPPSMI 60

Db 1 MSESPEALPSLGCVLVPVLLAGPRPAEGPRPSFWAMESQETEASVVLKCVKVSDFQPPSMI 60

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Db 61 EWYKNNKKIEQEKGIRVDIKDKYIHQKSLFYLRIVHLTEKDEGIYNCIGIIVGLEDTVQI 120

Qy 121 DLTVHSKPKITSFDSPTNVNEGKEVNLTCDAESKPEPTVSWWKDGVQLKKDNTLSLRHVT 180

Db 121 DLTVHSKPKITSFDSPTNVNEGKEVNLTCDAESKPEPTVSWWKDGVQLKKDNTLSLRHVT 180

Qy 181 RKHSGTYTCQGSHLYTELSSVVSLFVPVSQGASTTPAVHMDSDHLTILIFVTVVIILTLF 240

Db 181 RKHSGTYTCQGSHLYTELSSVVSLFVPVSQGASTTPAVHMDSDHLTILIFVTVVIILTLF 240

Qy 241 VLWIYKHRNRDRTIDESKRVDYDIHVNYSPAYSDPLQKSTRLSTDVMNMEAGNSSQPNSS 300

Db 241 VLWIYKHRNRDRTIDESKRVDYDIHVNYSPAYSDPLQKSTRLSTDVMNMEAGNSSQPNSS 300

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Db 301 DTGEEDIGETSYYCNQSVEGGIGNSTSTGRIIHGDSVLGLQPLAGNVKDPTLVSGSMDGP 360

Qy 361 RAPHLSLSPKSHLEIPTLSSSPQKSSPSLLSSTESKESSALYLGQLQTLRIADTALYICVP 420

Db 361 RAPHLSLSPKSHLEIPTLSSSPQKSSPSLLSSTESKESSALYLGQLQTLRIADTALYICVP 420

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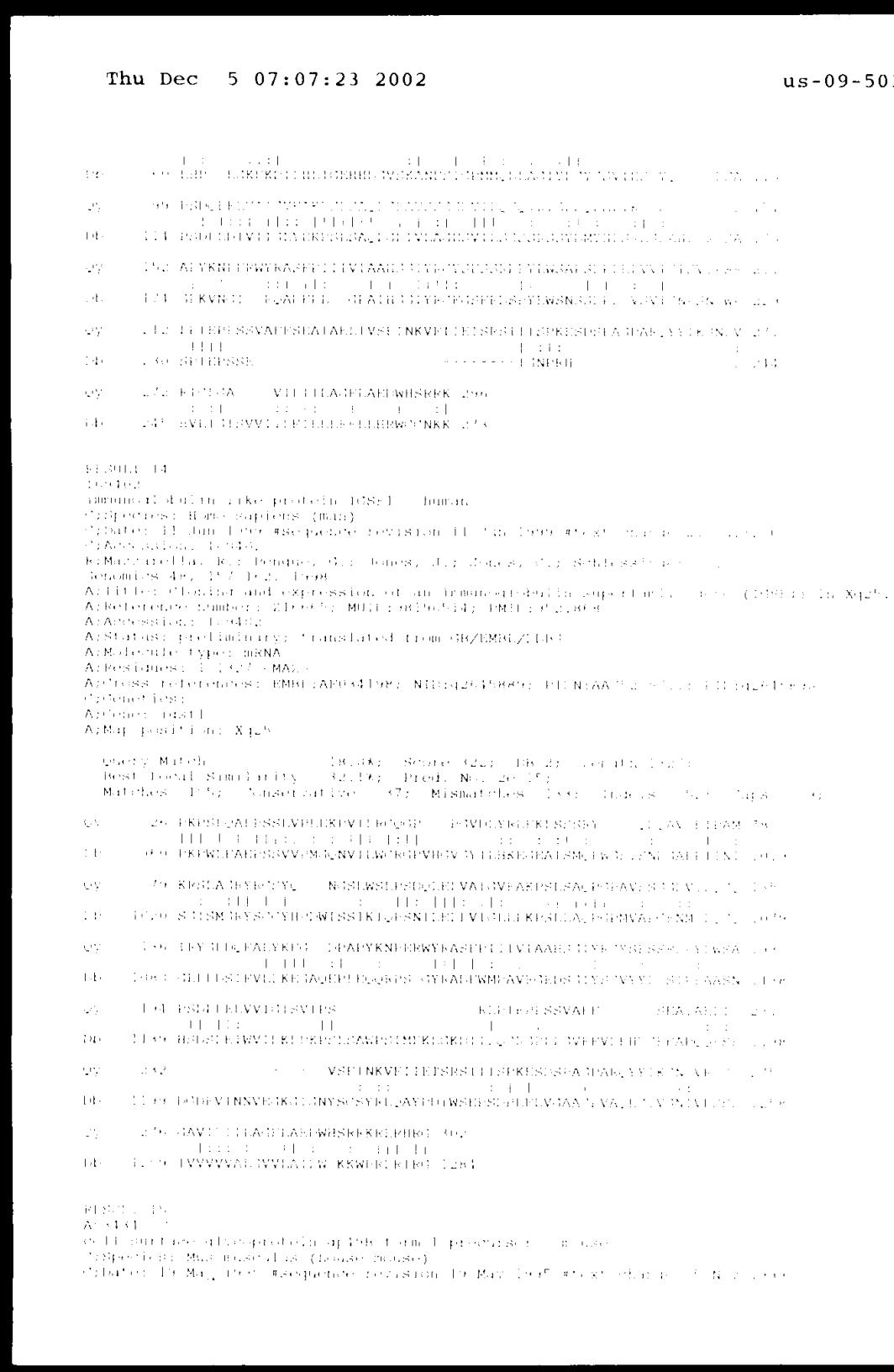

Mpi results - protein search, using sw model

Run started: December 5, 2002, 06:58:02 ; Search time 71 Seconds
(without alignments)
[illegible] Million cell updates/sec

Title: US-09-503-387-3

Perfect score: 1946

Sequence: 1 MSPSHALCVLGLCLSWEA..... ...KSCIL_GIPs_Vas 1 ...

Scoring table: BLOSUM62
Gap open 10.0 , Gap ext 0.5

Searched: 112892 seqs, 41479628 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt 40:*

The list N... of the number of results per database is [illegible] ... The scores are sorted by decreasing order of expect value (E), the probability of finding a match with a score greater than the score by chance in the database, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	592	21.9	287	1	[illegible]	[illegible]
2	542.5	19.2	387	1	[illegible]	[illegible]
3	448	16.0	672	1	[illegible]	[illegible]
4	445	16.8	444	1	[illegible]	[illegible]
5	436.5	16.5	864	1	[illegible]	[illegible]
6	425	15.4	843	1	[illegible]	[illegible]
7	420	15.4	340	2	[illegible]	[illegible]
8	420	15.2	674	1	[illegible]	[illegible]
9	420.5	15.1	711	2	[illegible]	[illegible]
10	420.5	15.9	864	1	[illegible]	[illegible]
11	414	15.3	455	1	[illegible]	[illegible]
12	417.5	15.8	855	1	[illegible]	[illegible]
13	412	15.2	864	1	[illegible]	[illegible]
14	394	14.7	804	1	[illegible]	[illegible]
15	390.5	14.2	363	1	[illegible]	[illegible]
16	312.5	8.0	474	1	[illegible]	[illegible]
17	140	7.8	291	1	[illegible]	[illegible]
18	136.5	7.1	4217	1	[illegible]	[illegible]
19	134.5	6.9	267	1	[illegible]	[illegible]
20	130	6.8	2774	1	[illegible]	[illegible]
21	125.5	6.5	2709	1	[illegible]	[illegible]
22	119	6.4	4193	1	[illegible]	[illegible]
23	123.5	6.4	1284	1	[illegible]	[illegible]
24	108	6.0	257	1	[illegible]	[illegible]
25	108	6.0	341	1	[illegible]	[illegible]
26	107	5.9	261	1	[illegible]	[illegible]
27	106.5	5.9	2481	1	[illegible]	[illegible]
28	106	5.9	285	1	[illegible]	[illegible]
29	106	5.9	739	1	[illegible]	[illegible]
30	106	5.9	2161	1	[illegible]	[illegible]
31	105.5	5.9	330	1	[illegible]	[illegible]
32	104	5.8	746	1	[illegible]	[illegible]
33	103	5.8	1002	1	[illegible]	[illegible]
34	103.5	5.8	[illegible]	1	[illegible]	[illegible]
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36	102.5	5.7	[illegible]	1	[illegible]	[illegible]
37	102	5.7	[illegible]	1	[illegible]	[illegible]
38	101	5.7	[illegible]	1	[illegible]	[illegible]
39	101	5.7	[illegible]	1	[illegible]	[illegible]
40	100.5	5.6	[illegible]	1	[illegible]	[illegible]
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42	99.5	5.6	[illegible]	1	[illegible]	[illegible]
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ALIGNMENTS

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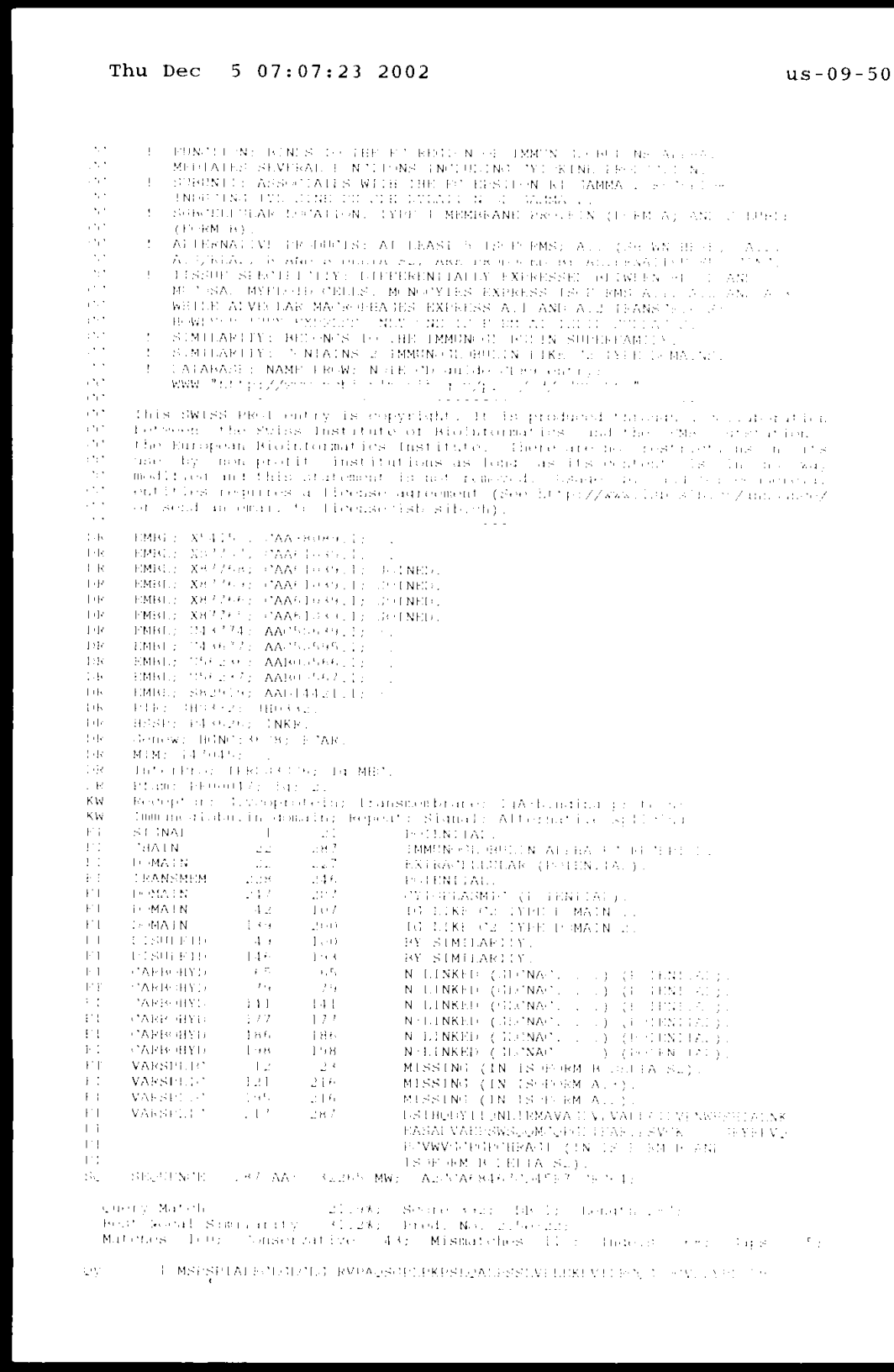
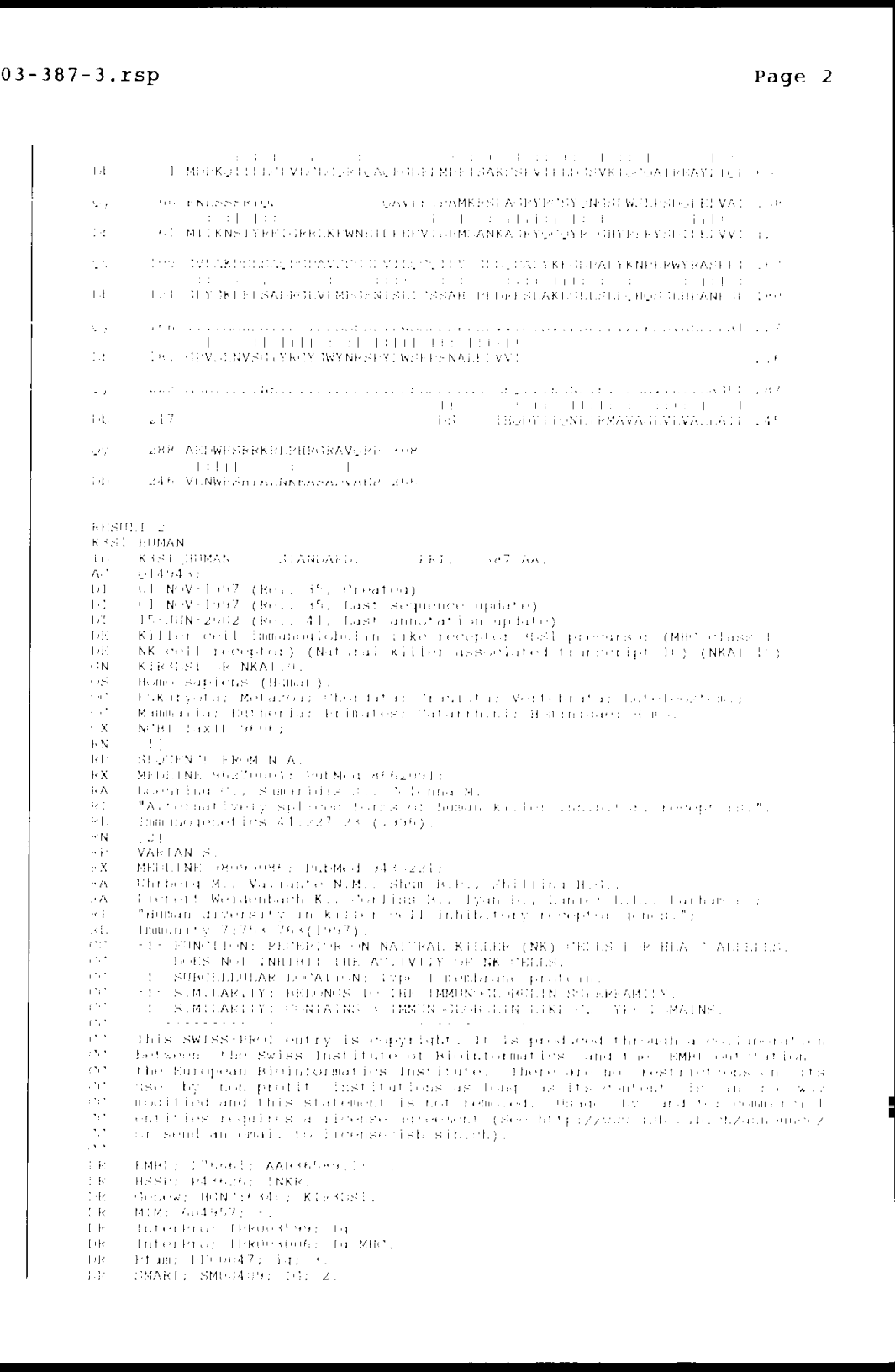
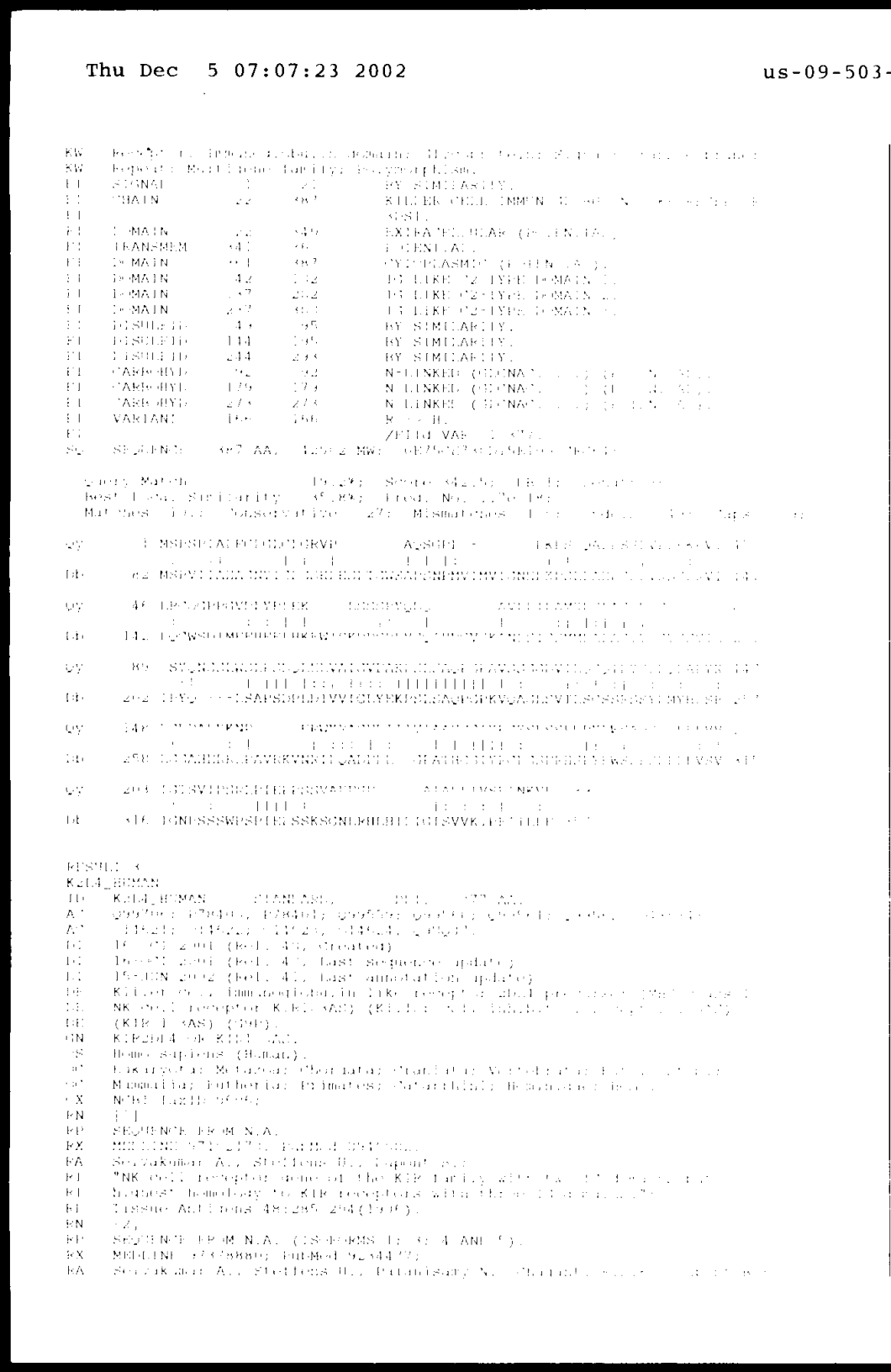
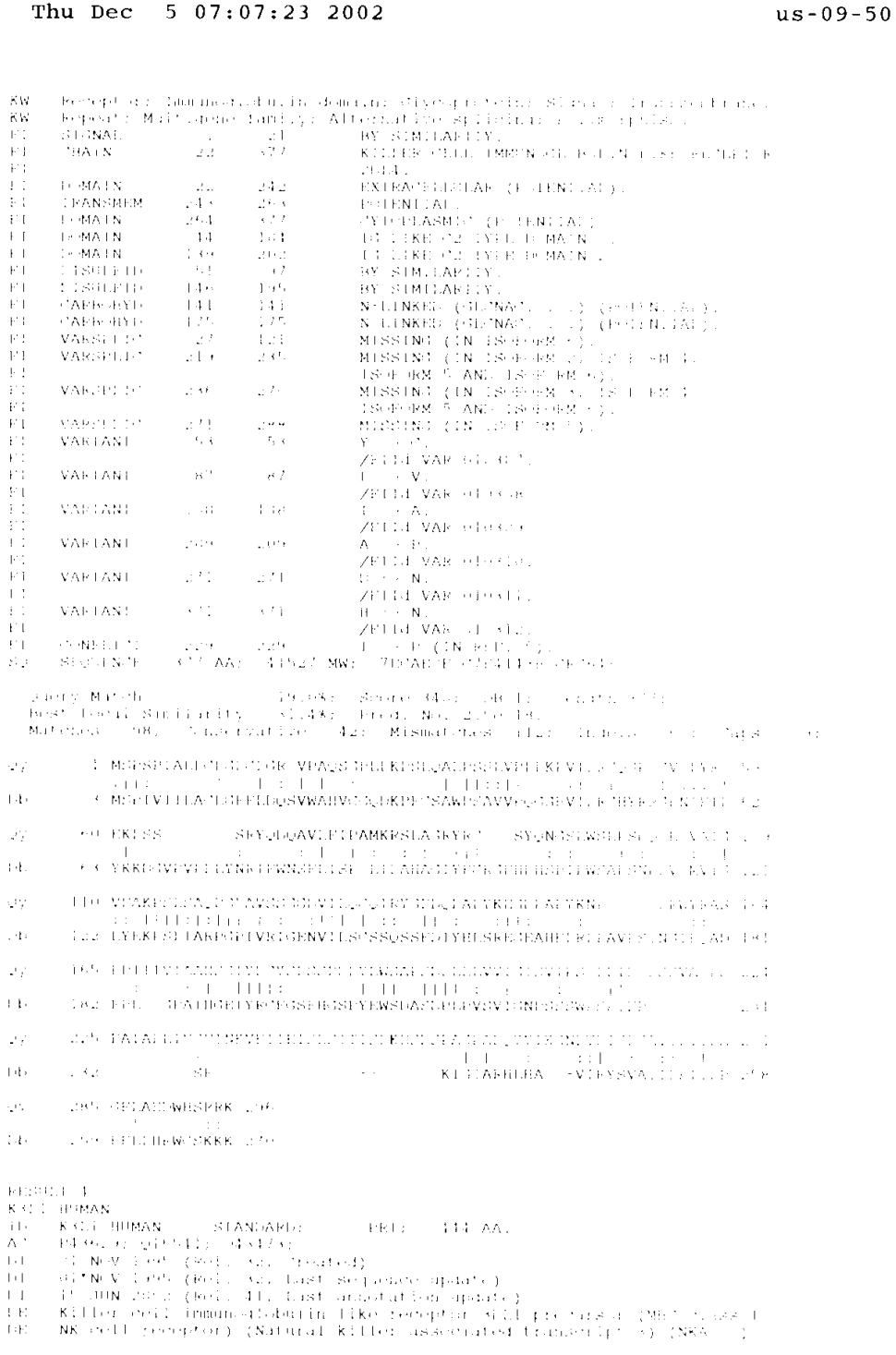
AC [illegible]; [illegible]; [illegible]; [illegible]; [illegible].
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Immunoglobulin alpha Fc receptor precursor (IgA Fc receptor) (FcaR)
DE (CD89).
GN [illegible].
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91079260; PubMed=2246504;
RA Maliszewski C.R., March C.J., Schoenborn M.A., Gimpel S., Shen L.;
RT "Expression cloning of a human Fc receptor for IgA.";
RL J. Exp. Med. 172:1665-1672(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96366084; PubMed=8764838;
RA de Wit T.P.M., Morton H.C., van Egmond M., Capel P.J.A., van de Winkel J.G.J.;
RT "Structure of the gene for the human myeloid IgA Fc receptor (CD89).";
RL J. Immunol. 157:1203-1209(1996).
RN [3]
RP SEQUENCE FROM N.A. (1) AND (2) (ISOFORMS A2 AND A3).
RC TISSUE=Alveolar macrophage and Monocyte;
RX MEDLINE=96127662; PubMed=8550383;
RA Pleyer U., Gillitzer R., Mackensen A., Moderegger E.;
RT "Identification of Fc alpha receptor (CD89) isoforms generated by
RT alternative splicing and differentially expressed between blood
RT monocytes and alveolar macrophages.";
RL J. Immunol. 156:4442-4448(1996).
RN [4]
RP SEQUENCE FROM N.A. (1) (ISOFORMS A2 AND A3).
RA van Dijk T.B., Mous R.A.C., Valdenebro F., Bracke M.,
RA Raijmakers J.A.M., Lammers J.-W.J., Koenderman L., Otten H.G.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (1) (ISOFORM A3).
RX MEDLINE=96345096; PubMed=8855186;
RA Pleyer U., Andrews P.W., Gillitzer R., Moore M.A., Steel D.M.;
RT "Alternative splicing of the human IgA Fc receptor CD89 in
RT neutrophils and eosinophils.";
RL Biochem. J. 318:771-777(1996).
RN [6]
RP SUBUNITS.
RX MEDLINE=91375887; PubMed=2072256;
RA Pfefferkorn L.C., Yeaman G.R.;
RT "Association of IgA Fc receptors (Fc alpha R) with Fc epsilon RI
RT gamma 2 subunits in U937 cells. Aggregation induces the tyrosine
RT phosphorylation of gamma 2."
RL J. Immunol. 147:1228-1236(1991).









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ID   KLRA_HUMAN     STANDARD;      PRT;   394 AA.
AC   P43631; Q14455;
DT   01-NOV-1995 (Rel. 32, Created)
DT   15-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Killer cell immunoglobulin-like receptor 2DL2 precursor (MHC class I
DE   NK cell receptor) (Natural killer associated transcript 2a (NKAT-2)
DE   (p58 natural killer cell receptor clone CL-4) (p58 NK receptor 1) (NK
DE   receptor 183.A*1).
GN   KIR2DS2 OR NKAT2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Natural killer cell;
RX   MEDLINE=96249128; PubMed=8774119;
RA   Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Malnati M.S.,
RA   Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT   "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RT   related molecules with diversity in both the extra- and intracellular
RT   domains.";
RL   Immunity 2:439-449(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoid;
RX   MEDLINE=96197217; PubMed=8611693;
RA   Biassoni R., Cantoni C., Falco M., Verdiani S., Bottino C., Vitale M.,
RA   Conte R., Pessi A., Moretta A., Moretta L.;
RT   "The human leukocyte antigen (HLA)-C-specific 'activatory' or
RT   'inhibitory' natural killer cell receptors display highly homologous
RT   extracellular domains but differ in their transmembrane and
RT   intracytoplasmic portions.";
RL   J. Exp. Med. 183:645-650(1996).
CC   -!- FUNCTION: RECEPTOR FOR HLA-C SPECIFIC NATURAL KILLER (NK) CELLS. BINDS
CC       TO HLA-C ALLELES.
CC   -!- DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2 TYPE DOMAINS.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   -----------------------------------------------------------------------
DR   EMBL; U24076; AAC50440.1; ALT_INIT.
DR   EMBL; L41347; AAA51...1;
DR   EMBL; X70029; CAA49...1; -.
DR   HSSP; P43626; 1NKB.
DR   Genew; HGNC:6334; KIR2...
DR   MIM; 604937; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
KW   Receptor; Immunoglobulin-like; Transmembrane; Glycoprotein; Signal; Repeat;
KW   Repeat; Multigene family.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    343       KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT                                 2DL2.
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FT   TRANSMEM     121   141       POTENTIAL.
FT   DOMAIN       142   343       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       142   202       IG-LIKE C2-TYPE 1 DOMAIN.
FT   DOMAIN       237   306       IG-LIKE C2-TYPE 2 DOMAIN.
FT   DISULFID     49    95        BY SIMILARITY.
FT   DISULFID     131   187       BY SIMILARITY.
FT   DISULFID     241   293       BY SIMILARITY.
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FT                                /FTId=VAR_001934.
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FT                                /FTId=VAR_001935.
FT   VARIANT      259   259       G -> E.
FT                                /FTId=VAR_001936.
FT   VARIANT      333   333       S -> P.
FT                                /FTId=VAR_001937.
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  Query Match             18.8%;  Score 335;  DB 1;  Length 414;
  Best Local Similarity   30.4%;  Pred. No. 7.5e-16;
  Matches  112;  Conservative   44;  Mismatches  127;  Indels   44;  Gaps   12;

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Qy       46 LPQPPDVHLLPPLTEPKDSLSGDFVQTKFQAV---- ----- IPTPAMKPSLHPEGRYR  98
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Qy       99 DVQWLFNGQVLPTDRVSNMVVETRRNRDLCLLATQNLRDSGAYSCRQRLTRSVLCHFEVRV  158
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Db      374 SLGMNPRAQDKVG  386


RESULT 5
KLRA_HUMAN
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ID   KLRA_HUMAN     STANDARD;      PRT;   394 AA.
AC   P43631; Q14455;
DT   01-NOV-1995 (Rel. 32, Created)
DT   15-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Killer cell immunoglobulin-like receptor 2DL2 precursor (MHC class I
DE   NK cell receptor) (Natural killer associated transcript 2a (NKAT-2)
DE   (p58 natural killer cell receptor clone CL-4) (p58 NK receptor 1) (NK
DE   receptor 183.A*1).
GN   KIR2DS2 OR NKAT2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Natural killer cell;
RX   MEDLINE=96249128; PubMed=8774119;
RA   Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Malnati M.S.,
RA   Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT   "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RT   related molecules with diversity in both the extra- and intracellular
RT   domains.";
RL   Immunity 2:439-449(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoid;
RX   MEDLINE=96197217; PubMed=8611693;
RA   Biassoni R., Cantoni C., Falco M., Verdiani S., Bottino C., Vitale M.,
RA   Conte R., Pessi A., Moretta A., Moretta L.;
RT   "The human leukocyte antigen (HLA)-C-specific 'activatory' or
RT   'inhibitory' natural killer cell receptors display highly homologous
RT   extracellular domains but differ in their transmembrane and
RT   intracytoplasmic portions.";
RL   J. Exp. Med. 183:645-650(1996).
CC   -!- FUNCTION: RECEPTOR FOR HLA-C SPECIFIC NATURAL KILLER (NK) CELLS. BINDS TO HLA-C ALLELES.
CC   -!- DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2 TYPE DOMAINS.
CC   -----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; U24076; AAC50440.1; ALT_INIT.
DR   EMBL; L41347; AAA51...1;
DR   EMBL; X70029; CAA49...1; -.
DR   HSSP; P43626; 1NKB.
DR   Genew; HGNC:6334; KIR2...
DR   MIM; 604937; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
KW   Receptor; Immunoglobulin-like; Transmembrane; Glycoprotein; Signal; Repeat;
KW   Repeat; Multigene family.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    343       KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT                                 2DL2.
FT   DOMAIN       22    120       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     121   141       POTENTIAL.
```

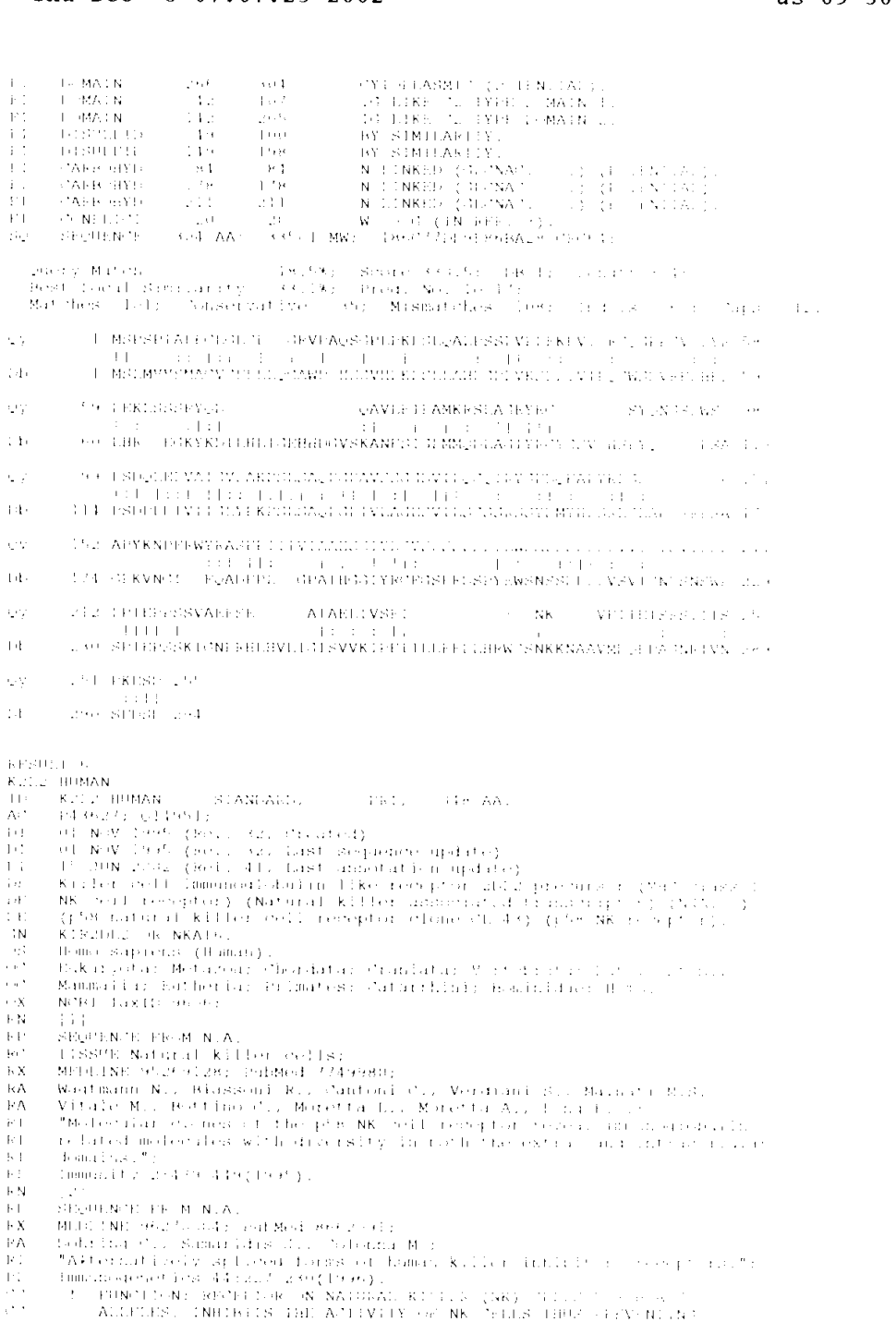

```
ID   S? N-V [**] (Rel. **, Created)
DC   ** N-V [**] (Rel. **, Last sequence update)
DC   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Killer cell immunoglobulin-like receptor 2 DL3 precursor (KIR2DL3)
DE   (NK cell receptor) (Natural killer associated transcript 2) (NKAT-2)
DE   (p58 natural killer cell receptor clone GL183 p58-) (CD158b)
DE   precursor) (p58.2 MHC class I specific NK receptor 1).
GN   KIR2DL3 OR NKAT2 OR CD158B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [**]
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=NK cell;
RX   MEDLINE=**; PubMed=**;
RA   Colonna M., Samaridis J.;
RT   "Cloning of immunoglobulin-superfamily members associated with HLA
RT   and MHC class I recognition by human natural killer cells.";
RL   Science 268:405-408(1995).
RN   [2]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 22-47.
RC   TISSUE=Natural killer cell;
RX   MEDLINE=**; PubMed=**;
RA   Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Malnati M.S.,
RA   Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT   "Molecular clones of the p58 NK cell receptor reveal immunoglobulin
RT   related molecules with diversity in both the extracellular and the
RC   domains.";
RL   Immunity 2:439-449(1995).
RN   [3]
RP   SEQUENCE FROM N.A., AND VARIANTS.
RX   MEDLINE=**; PubMed=**;
RA   Uhrberg M., Valiante N.M., Shum B.P., Shilling H.G.,
RA   Lienert-Weidenbach K., Corliss B., Tyan D., Lanier L.L., Parham P.;
RT   "Human diversity in killer cell inhibitory receptor genes.";
RL   Immunity 7:753-763(1997).
RN   [4]
RP   [illegible]
RX   MEDLINE=**; PubMed=**;
RA   Fan Z.T., Mesyak L., Winter C.C., Wagtmann N., [illegible]
RT   "Structure of the inhibitory receptor for human natural killer cells
RT   resembles haematopoietic receptors.";
RL   Nature **:**-** (1997).
CC   -!- FUNCTION: RECEPTOR FOR NATURAL KILLER (NK) CELLS. [illegible]
CC       INHIBITS THE ACTIVITY OF NK CELLS UPON BINDING [illegible]
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE [illegible]
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a [illegible]
CC   between the Swiss Institute of Bioinformatics and the [illegible]
CC   the European Bioinformatics Institute. There are [illegible] on its
CC   use by non-profit institutions as [illegible]. See [illegible]
CC   modified and this statement is not removed. Usage [illegible]
CC   entities requires a license agreement (See http://www.isb-[illegible]/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; L41267; AAA59[illegible].1; -.
DR   EMBL; U24076; AAC50355.1; -.
DR   EMBL; U24078; AAC50357.1; -.
DR   EMBL; AF022945; AAB95418.1; -.
DR   HSSB; [illegible]; 1-NOV-98.
DR   GeneCards; GC19P054992; KIR2DL3.
DR   MIM; 604946; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   InterPro; IPR[illegible]; Ig_like.
DR   Pfam; PF07686; Ig; 2.
DR   SMART; SM00406; IG; 1.
DR   SMART; SM00408; IGc2_like; 1.
KW   Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW   Repeat; Multigene family; Polymorphism; [illegible]

FT   SIGNAL          1     21
FT   CHAIN          22    346       KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT                                   2DL3.
FT   DOMAIN         22    117       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      246    268       POTENTIAL.
FT   DOMAIN        269    346       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN         42    117       IG-LIKE C2-TYPE 1 DOMAIN.
FT   DOMAIN        142    227       IG-LIKE C2-TYPE 2 DOMAIN.
FT   DISULFID       46    [illegible]
FT   DISULFID      149    [illegible]
FT   CARBOHYD       67     67       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD       81     81       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      131    131       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      178    178       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARIANT         5      5       V -> F.
FT                                   /FTId=VAR_009414.
FT   VARIANT        37     37       S -> R.
FT                                   /FTId=VAR_009415.
FT   VARIANT       135    135       I -> L.
FT                                   /FTId=VAR_009416.
FT   VARIANT       175    175       I -> S.
FT                                   /FTId=VAR_010033.
FT   VARIANT       181    181       I -> N.
FT                                   /FTId=VAR_010034.
FT   VARIANT       203    203       H -> R.
FT                                   /FTId=VAR_010035.
FT   VARIANT       237    237       K -> E.
FT                                   /FTId=VAR_010036.
FT   VARIANT       266    266       R -> C.
FT                                   /FTId=VAR_010037.
SQ   SEQUENCE   448 AA;  [illegible] MW;  [illegible]

  Query Match              10.4%;  Score 528;  DB 1;  Length 448;
  Best Local Similarity    [illegible]%;  Pred. No. 1.8e-27;
  Matches  [illegible];  Conservative   43;  Mismatches  [illegible];  Indels   84;  Gaps   11;

Qy       1 MSTSHLLGAGFLMLLQ [illegible]

Db      [illegible]

Qy      [illegible]

Db      [illegible]

Qy      [illegible]

Db      [illegible]

Qy      [illegible]

Db      [illegible]

Qy      [illegible]

Db      [illegible]

Qy      [illegible]

Db      [illegible]

Qy      [illegible]

Db      [illegible]

RESULT 8
KIR3_HUMAN
ID   KIR3_HUMAN     STANDARD;      [illegible]  AA.
AC   [illegible];
DT   16-[illegible]-2001 (Rel. 4[illegible], Created)
DT   16-[illegible]-2001 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Killer cell immunoglobulin-like receptor 2DL3 precursor (MHC class I
DE   NK cell receptor abc Ab1.).
GN   KIR-DL3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
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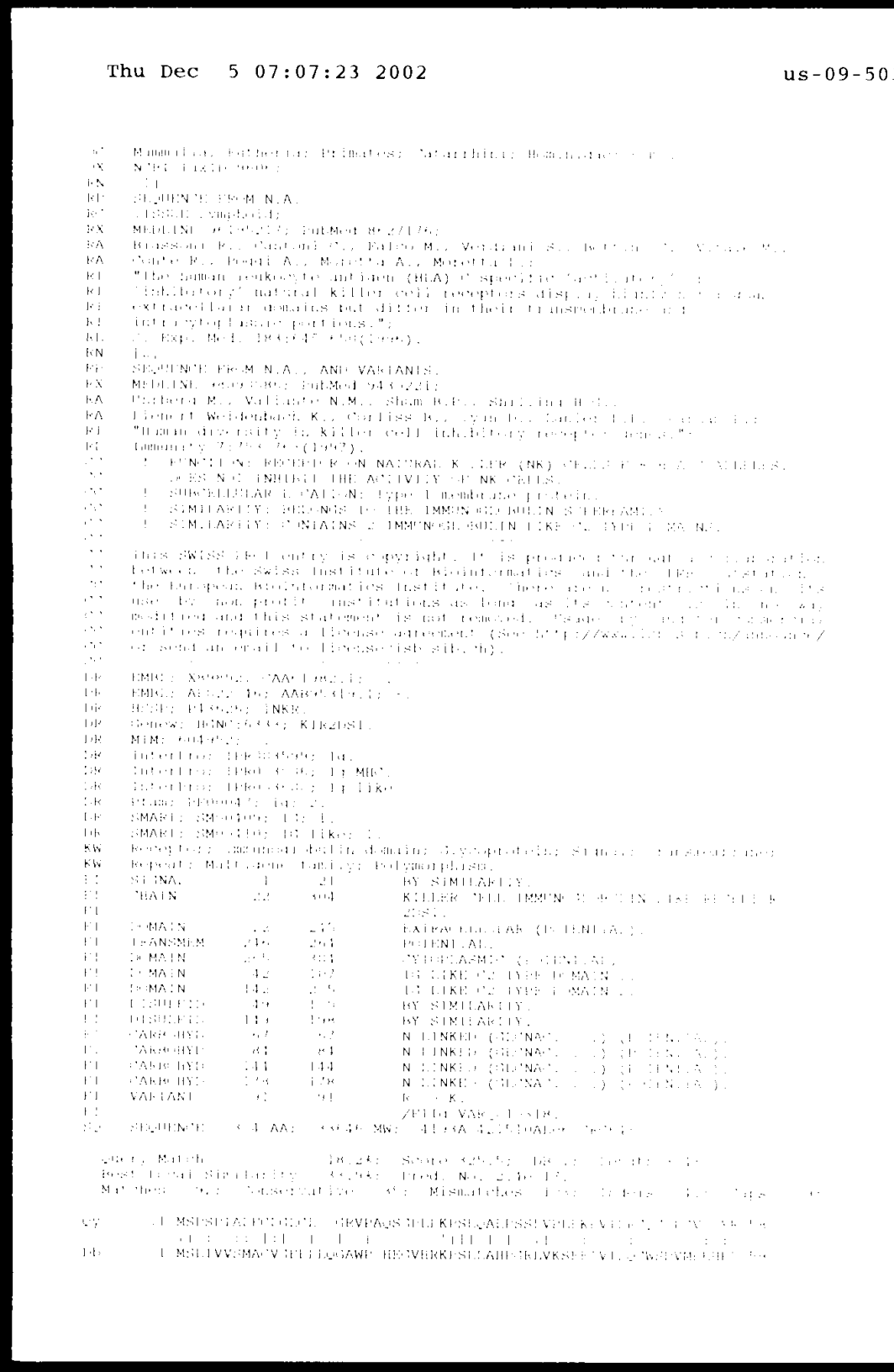
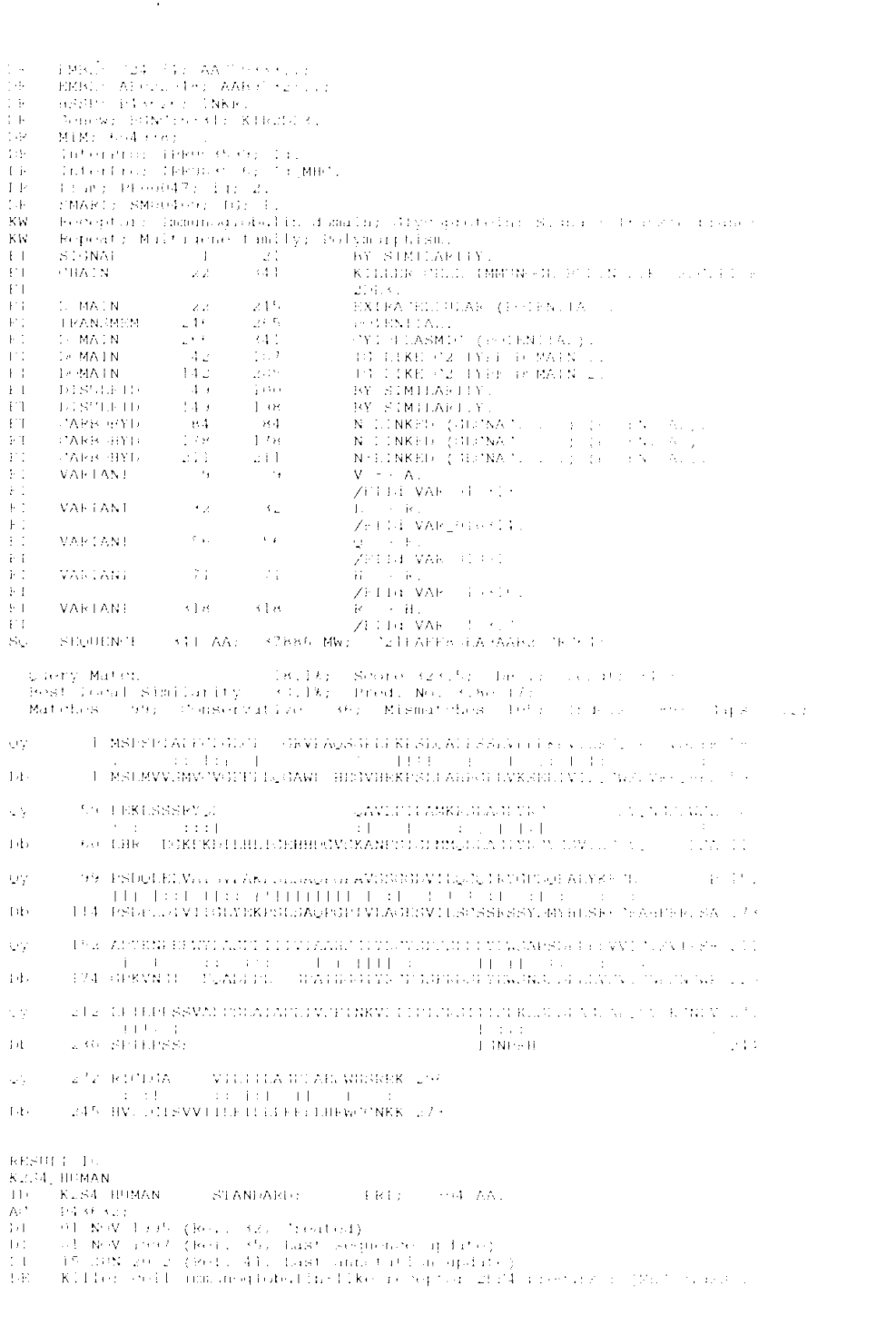
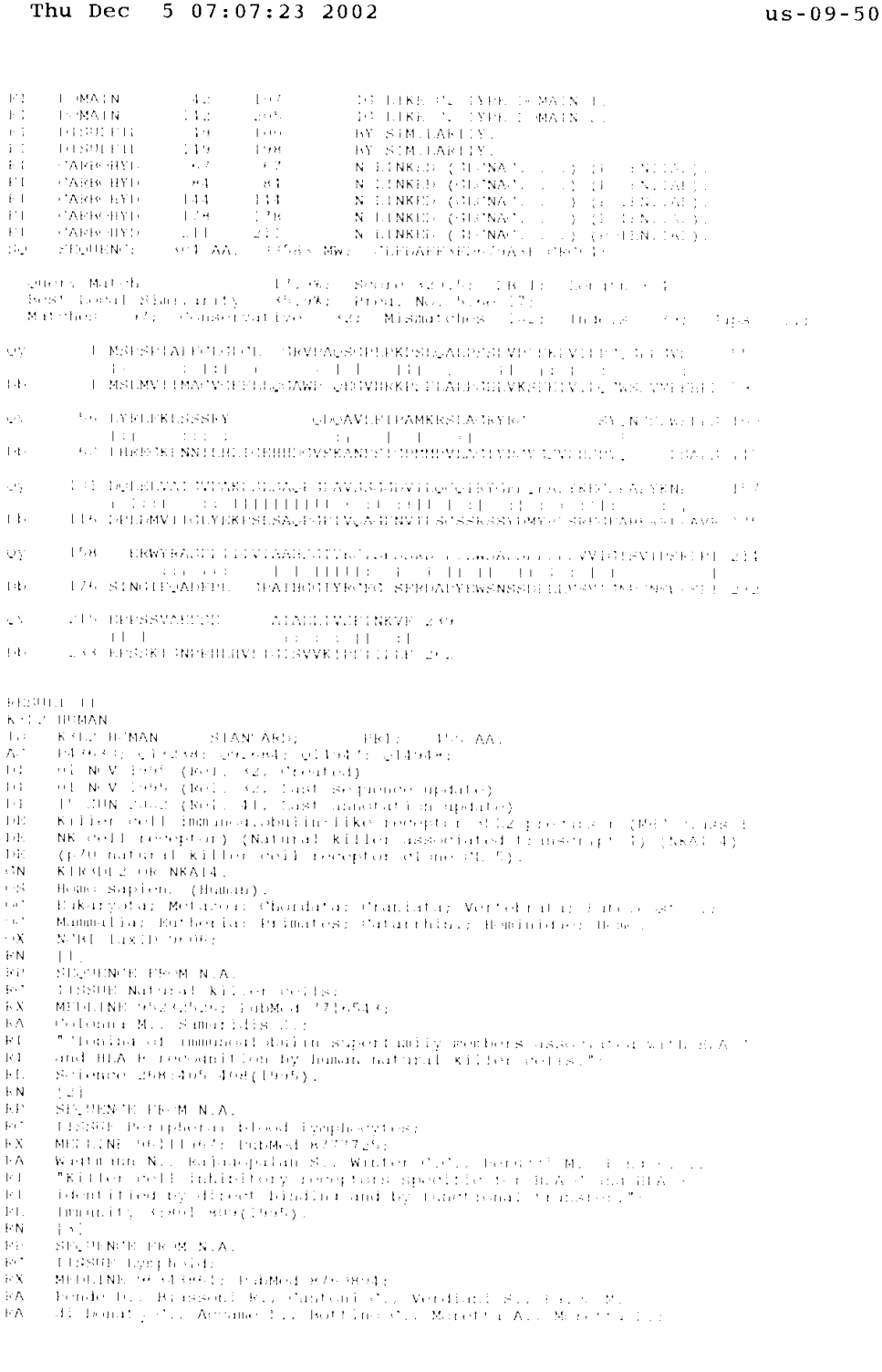
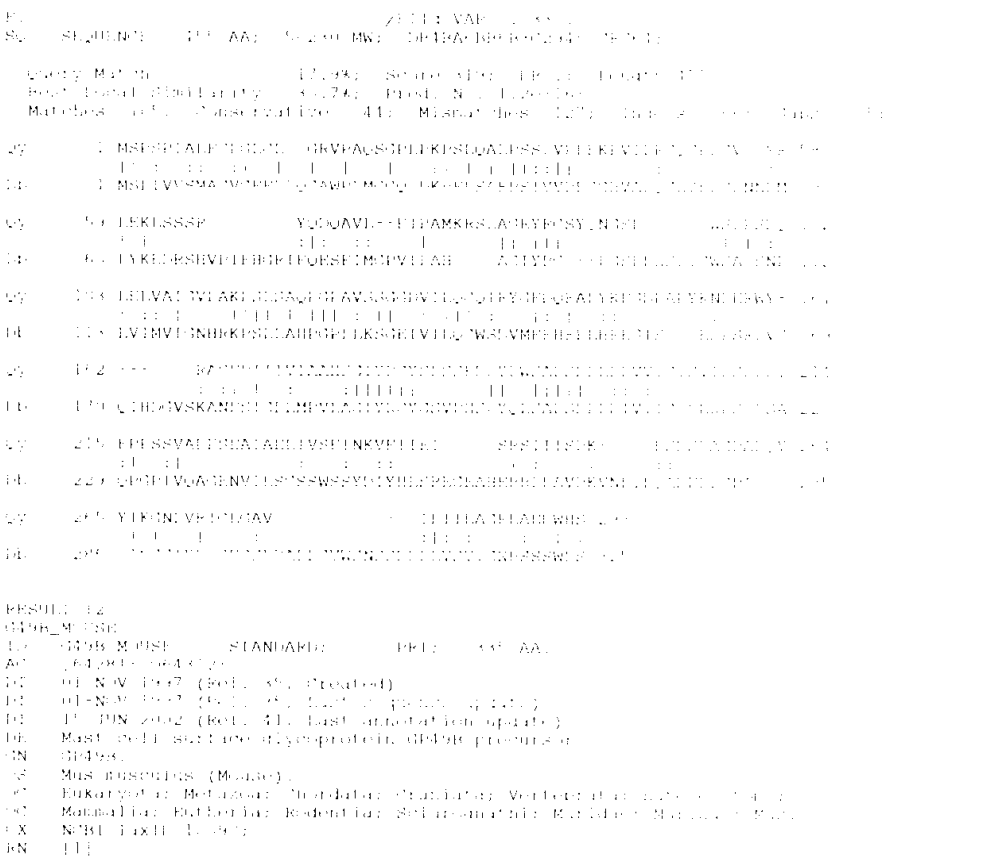
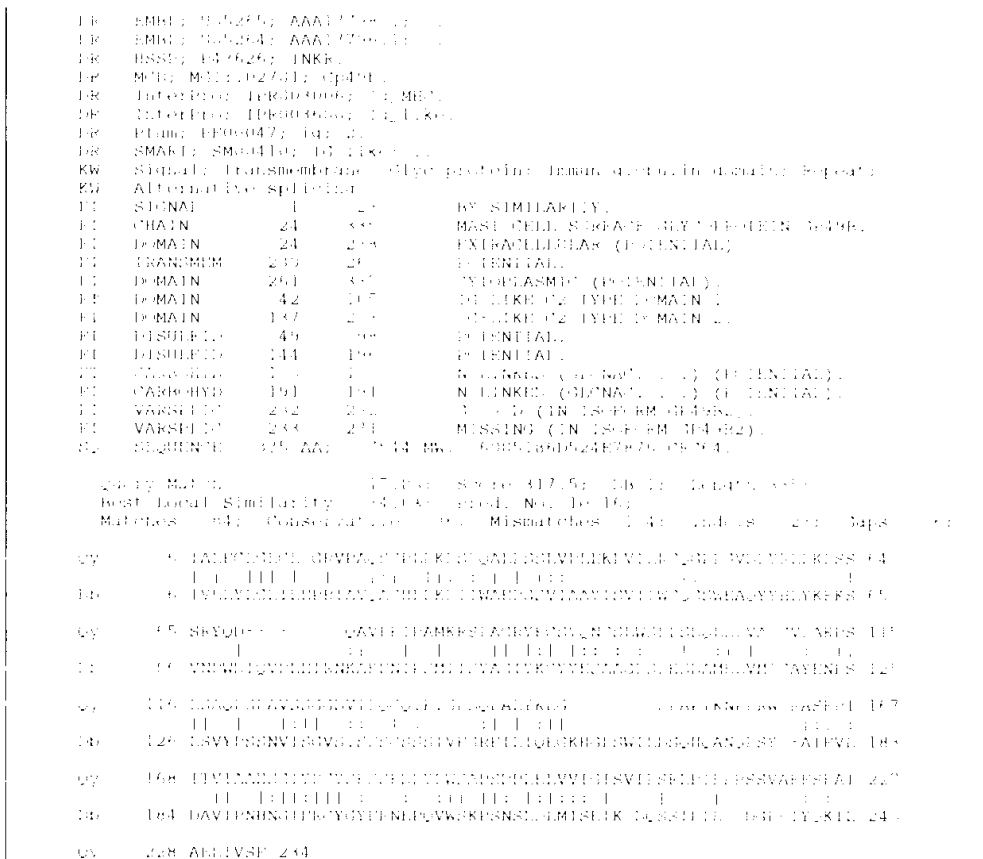
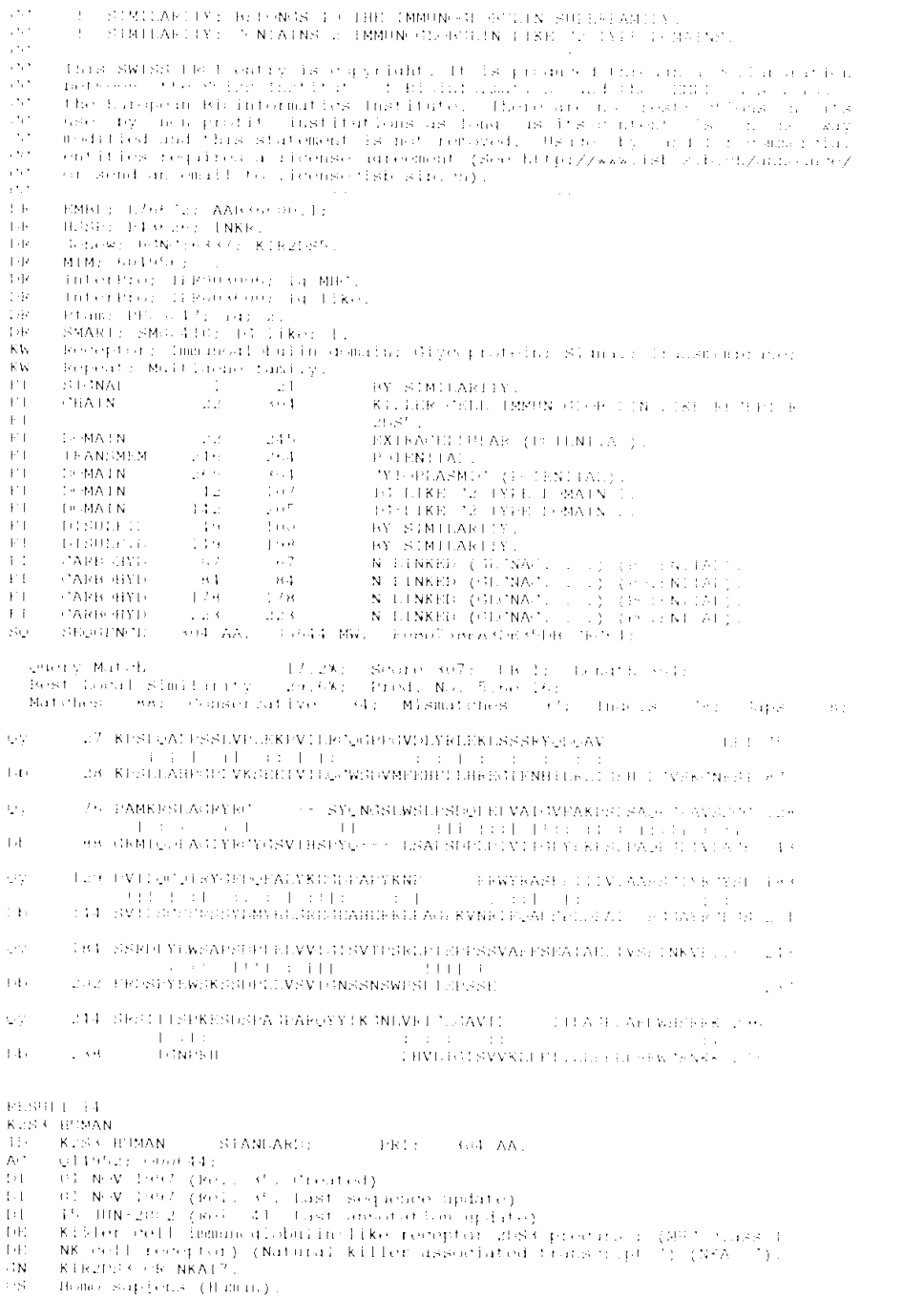


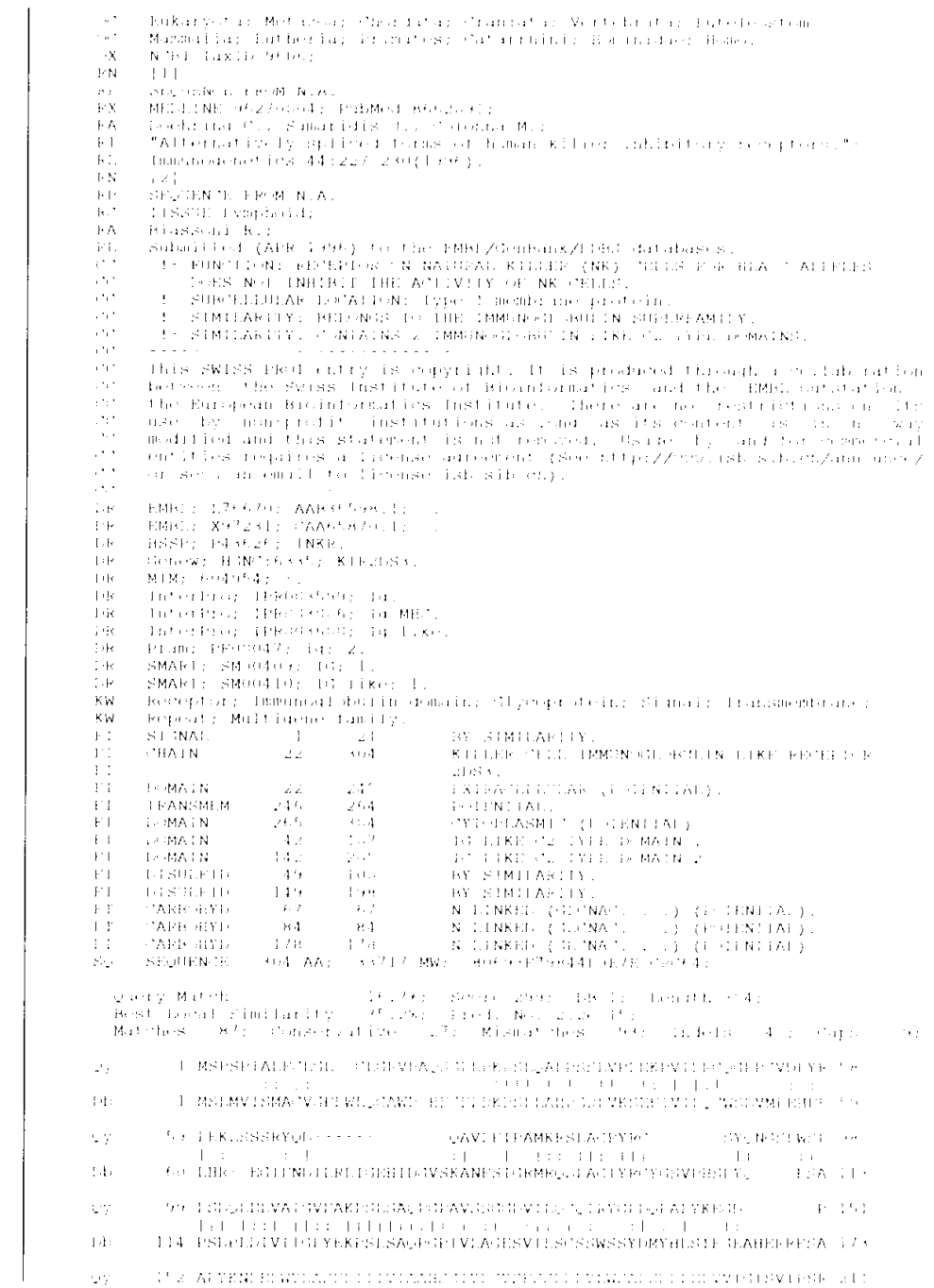


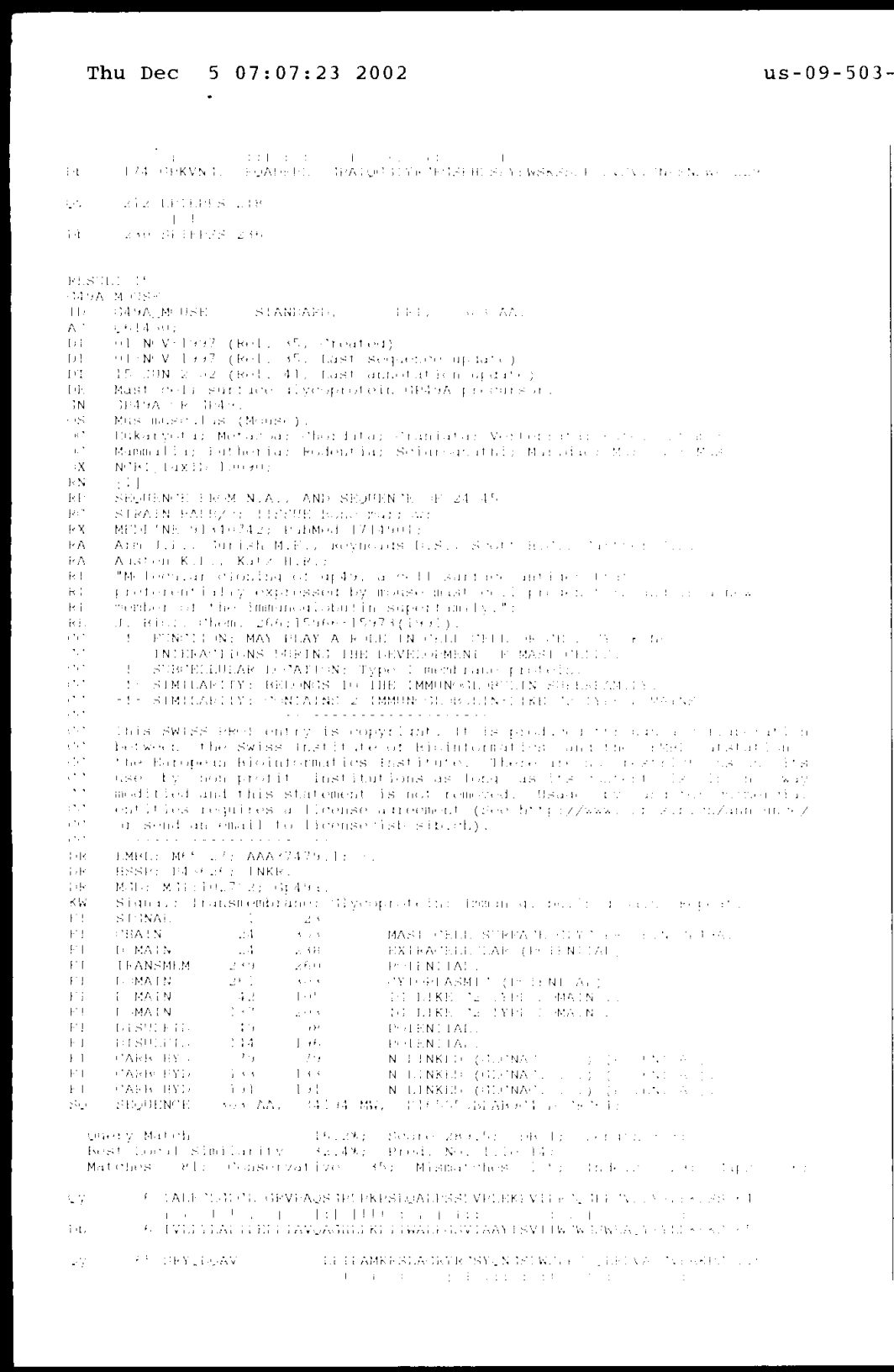












SM protein - protein search, using sw model

Run on: December 5, 2002, 06:52:46 ; Search time 41.2 Seconds
(without alignments)
2054.421 Million cell updates/sec

Title: US-09-503-387-3
Perfect score: 1794
Sequence: 1 MSPSPIALECLSLCLCRVFA.....KSEIQLSSS Length 570

Scoring matrix: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 67568 seqs, 29048217 residues

Total number of hits satisfying chosen parameters: 67568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_prions:*
16: sp_bacteriom:*
17: sp_archaeop:*

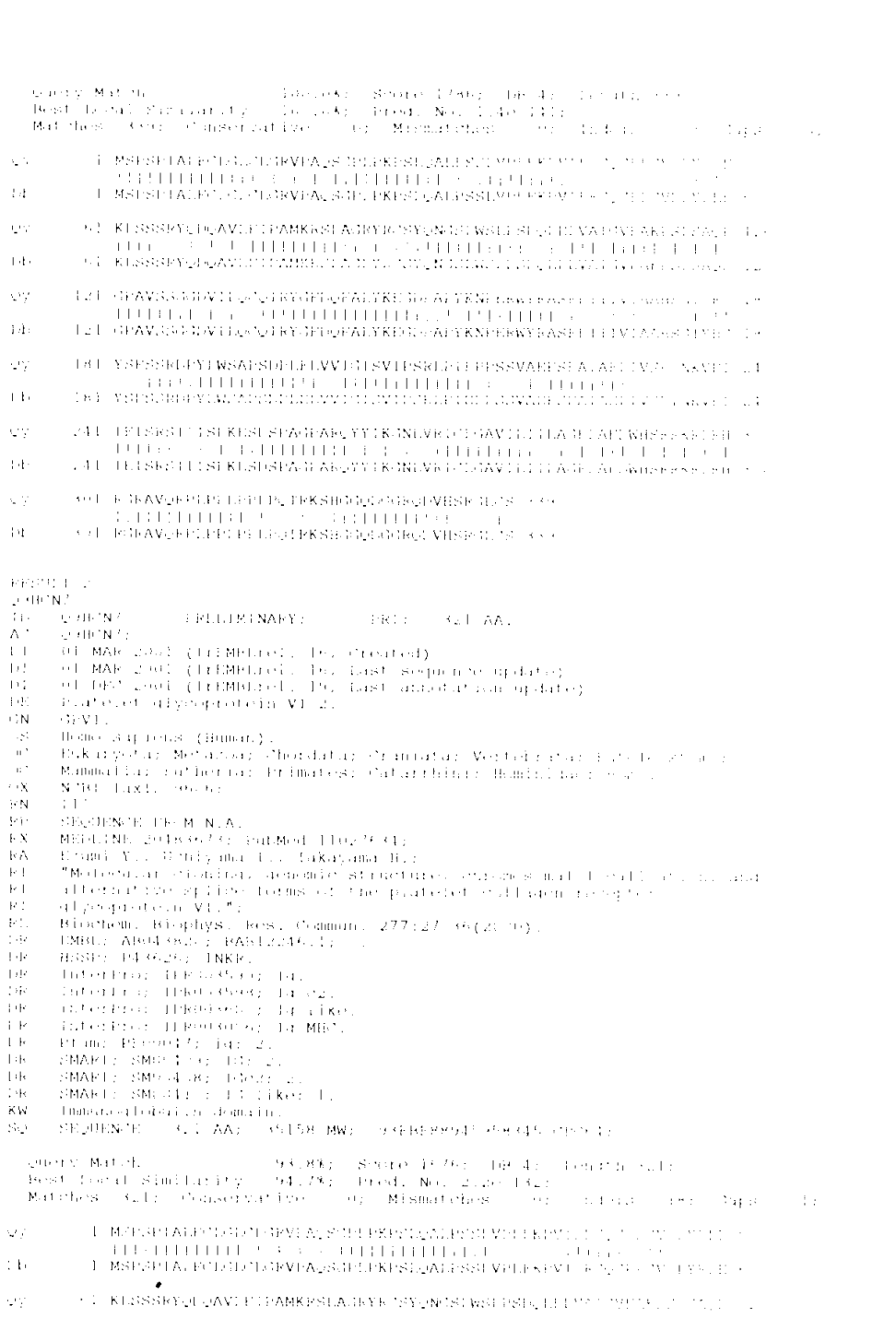
Pred. No. is the number of results predicted to occur in a database of this size with a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

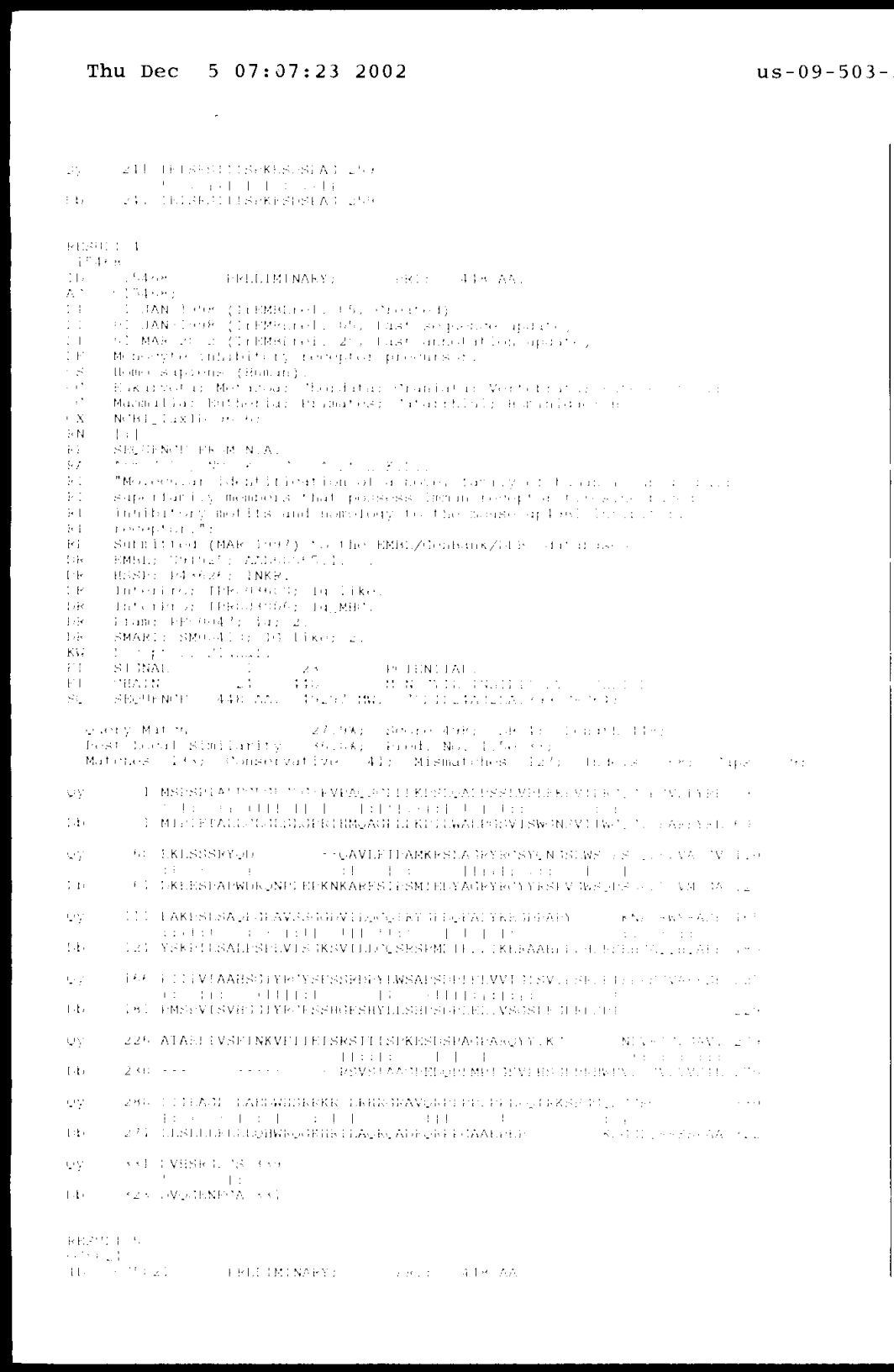
SUMMARIES

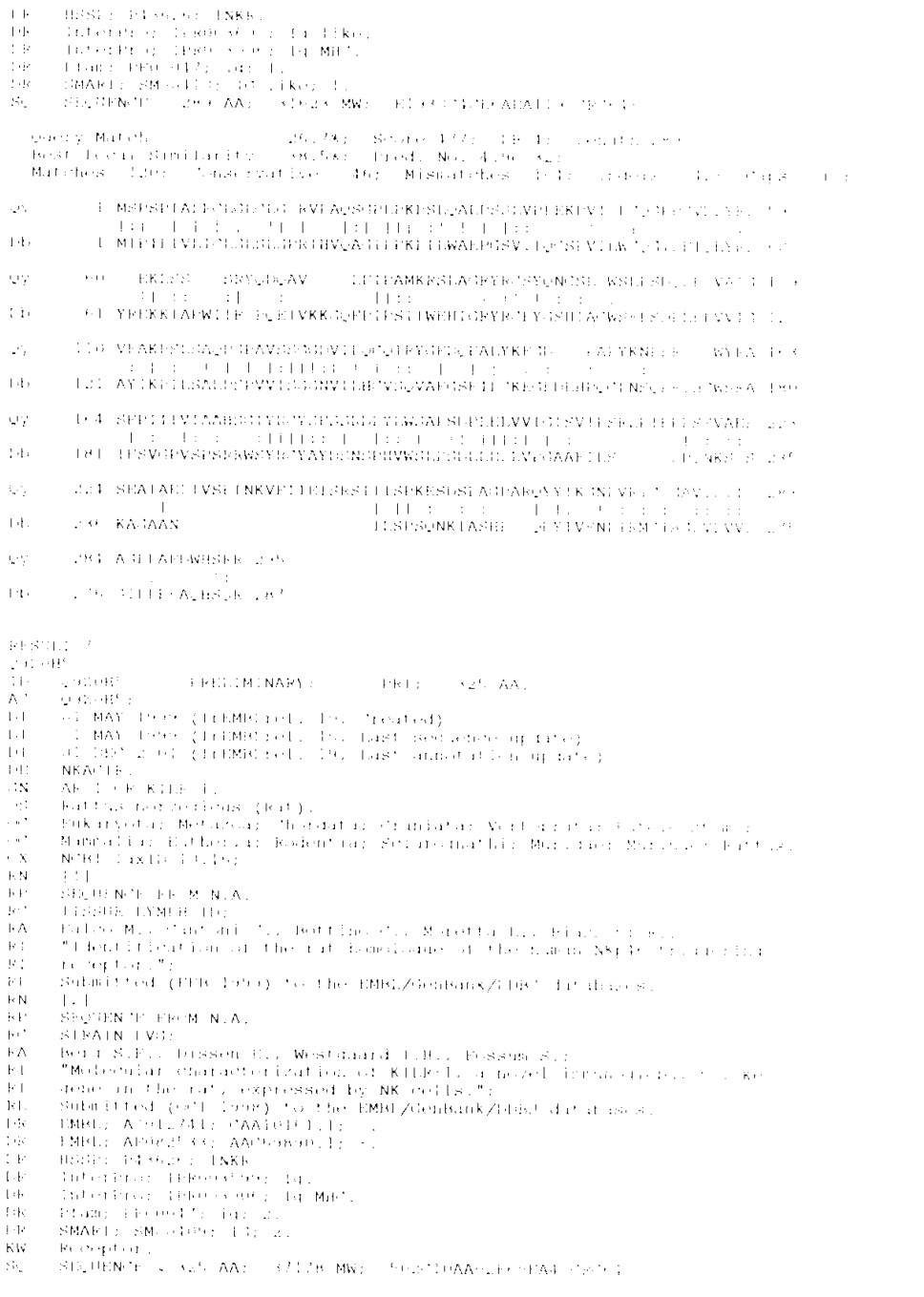
Result No.	Score	Query Match	Length	DB	ID	Description
1	1788	100.0	570	4	Q6GTE2	Q6GTE2 Homo sapien
2	1625	90.8	521	4	Q6HCN7	Q6HCN7 Homo sapien
3	1455	81.1	622	4	Q6HCN9	Q6HCN9 Homo sapien
4	1308	73.2	446	4	Q1F4P0	Q1F4P0 Homo sapien
5	1306	72.9	446	4	Q75PL1	Q75PL1 Homo sapien
6	837	46.8	289	4	Q75QJ8	Q75QJ8 Homo sapien
7	819	45.8	525	11	Q9Z0B5	Q9Z0B5 Mus musculus
8	815	45.4	504	4	Q7Z6J6	Q7Z6J6 Homo sapien
9	805	44.9	526	11	Q9Z2Q4	Q9Z2Q4 Mus musculus
10	804	44.8	641	4	Q75QJ1	Q75QJ1 Homo sapien
11	804	44.8	641	4	Q75QJ2	Q75QJ2 Homo sapien
12	417.5	23.3	287	4	Q7Z6J5	Q7Z6J5 Homo sapien
13	411	22.9	484	4	Q75QJ0	Q75QJ0 Homo sapien
14	410.5	22.9	409	4	Q9Z1B9	Q9Z1B9 Rattus rat
15	408.5	22.8	488	4	Q75QJ9	Q75QJ9 Homo sapien
16	381	21.3	508	4	Q75QJ7	Q75QJ7 Homo sapien
17	429	23.9	544	4	Q9Z0Z8	Q9Z0Z8 Homo sapien
18	426.5	23.8	541	4	Q9Z1P0	Q9Z1P0 Rattus
19	425.5	23.8	66	4	Q7Z7Q1	Q7Z7Q1 Homo sapien
20	422	23.6	669	4	Q9Z0Q6	Q9Z0Q6 Mus musculus
21	421.5	23.6	544	4	Q7Z7Q6	Q7Z7Q6 Homo sapien
22	418.5	23.4	410	4	Q7Z7G9	Q7Z7G9 Homo sapien
23	408.5	22.8	406	4	Q7Z7J6	Q7Z7J6 Homo sapien
24	407	22.7	41.	4	Q7Z7Q0	Q7Z7Q0 Homo sapien
25	372.5	20.8	441	11	Q9R2Z1	Q9R2Z1 Mus musculus
26	367.5	20.5	656	11	Q9Z0Q2	Q9Z0Q2 Mus musculus
27	362.5	20.3	831	11	Q9Z0Q9	Q9Z0Q9 Mus musculus
28	358	20.0	58.	2	Q7Z7J4	Q7Z7J4 Mus musculus
29	356.5	20.0	666	11	Q9Z0Q1	Q9Z0Q1 Mus musculus
30	351	19.7	279	4	Q7Z7K0	Q7Z7K0 Homo sapien
31	347.5	19.5	247	4	Q7Z7G5	Q7Z7G5 Homo sapien
32	343.5	19.2	98.	1	Q7Z7G9	Q7Z7G9 Homo sapien
33	342.5	19.2	98.	1	Q7Z7Q3	Q7Z7Q3 Homo sapien
34	340	19.0	419	1	Q7Z7W6	Q7Z7W6 Homo sapien
35	340	19.0	411	1	Q7Z7K1	Q7Z7K1 Homo sapien
36	338.5	18.9	96.	4	Q7Z7G4	Q7Z7G4 Homo sapien
37	338	18.9	95.	11	Q9Z7B4	Q9Z7B4 Mus musculus
38	332.5	18.6	414	1	Q9BER2	Q9BER2 Homo sapien
39	332	18.6	512	1	Q7Z7Q8	Q7Z7Q8 Homo sapien
40	329	18.4	111	1	Q7Z7Q9	Q7Z7Q9 Homo sapien
41	328	18.4	111	1	Q7Z7R0	Q7Z7R0 Homo sapien
42	327.5	18.3	52.	4	Q7Z7U2	Q7Z7U2 Homo sapien
43	327	18.3	51.	1	Q7Z7S4	Q7Z7S4 Homo sapien
44	326.5	18.3	201	7	Q7Z7H9	Q7Z7H9 Homo sapien
45	325.5	18.1	229	4	Q7Z7S1	Q7Z7S1 Homo sapien

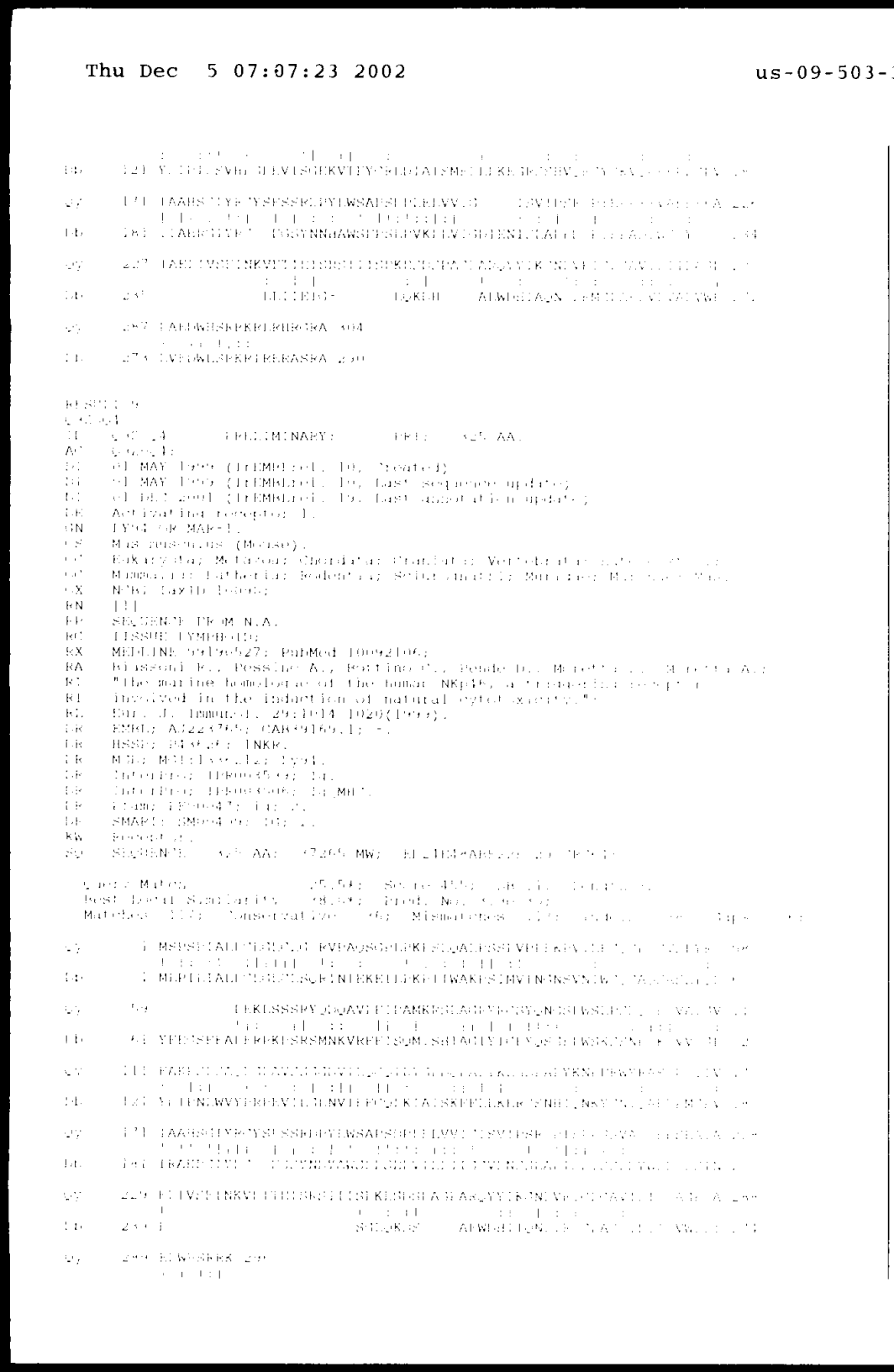
ALIGNMENTS

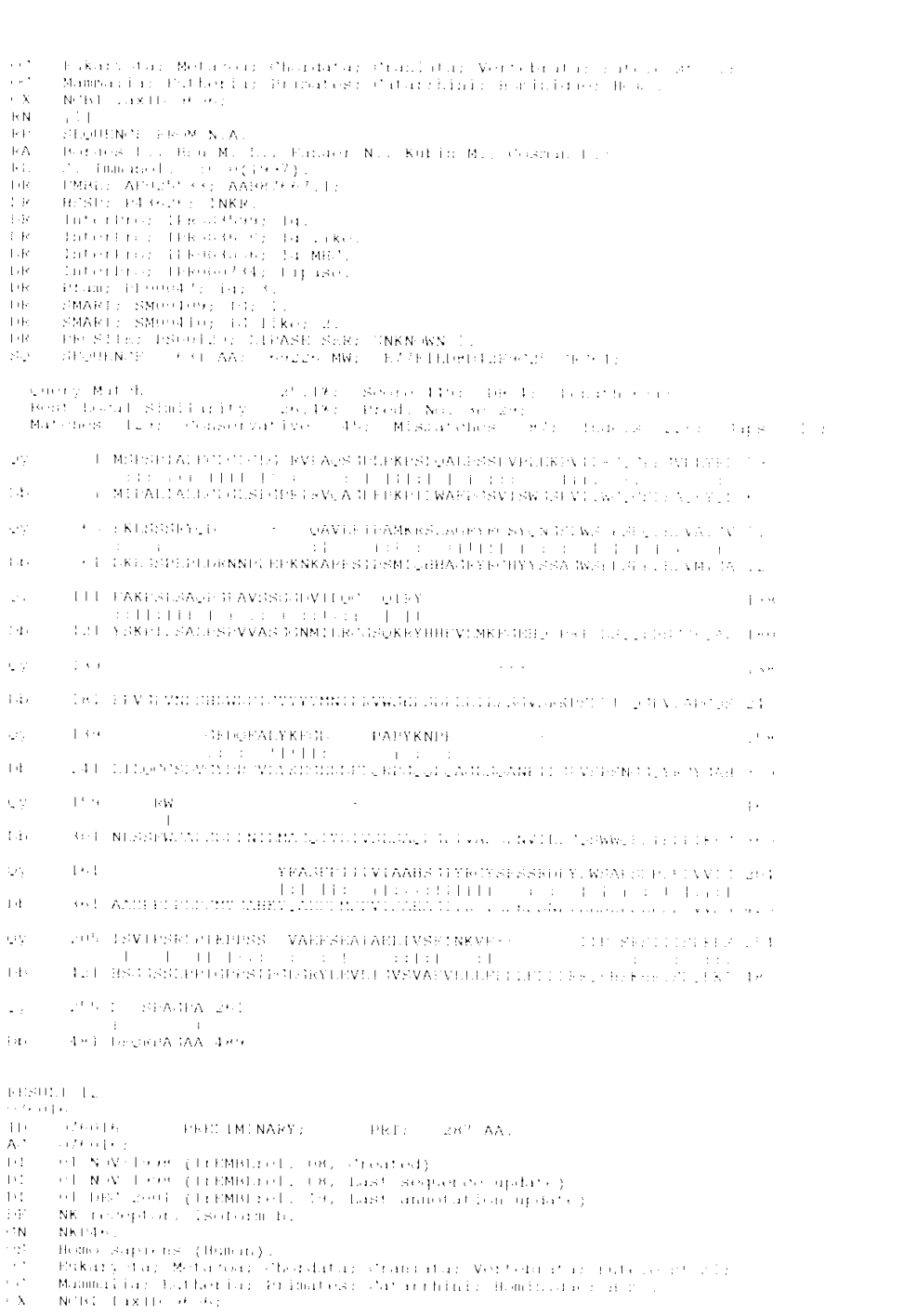
RESULT 1
Q6GTE2
ID Q6GTE2 PRELIMINARY; PRT; 570 AA.
AC Q6GTE2;
DT 01-MAY-2004 (TrEMBLrel. 23, Created)
DT 01-MAY-2004 (TrEMBLrel. 23, Last sequence update)
DT 01-DEC-2004 (TrEMBLrel. 26, Last annotation update)
DE Platelet glycoprotein VI precursor (Platelet glycoprotein VI 2)
GN GPVI
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Miura Y.;
RT "Platelet glycoprotein VI.";
RL Submitted (NOV 1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=12027634;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structures, chromosomal localization and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI.";
RL Biochem. Biophys. Res. Commun. 297:727-736(2002).
DR EMBL; AB050779; BAA82513.1; -.
DR EMBL; AB043819; BAB21845.1; -.
DR BSSP; 1390.6; INKR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00410; IG_like; 1.
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 570 POTENTIAL.
SQ SEQUENCE 570 AA; 62625 MW; 42A7C76B95E4C6C7 CRC64;

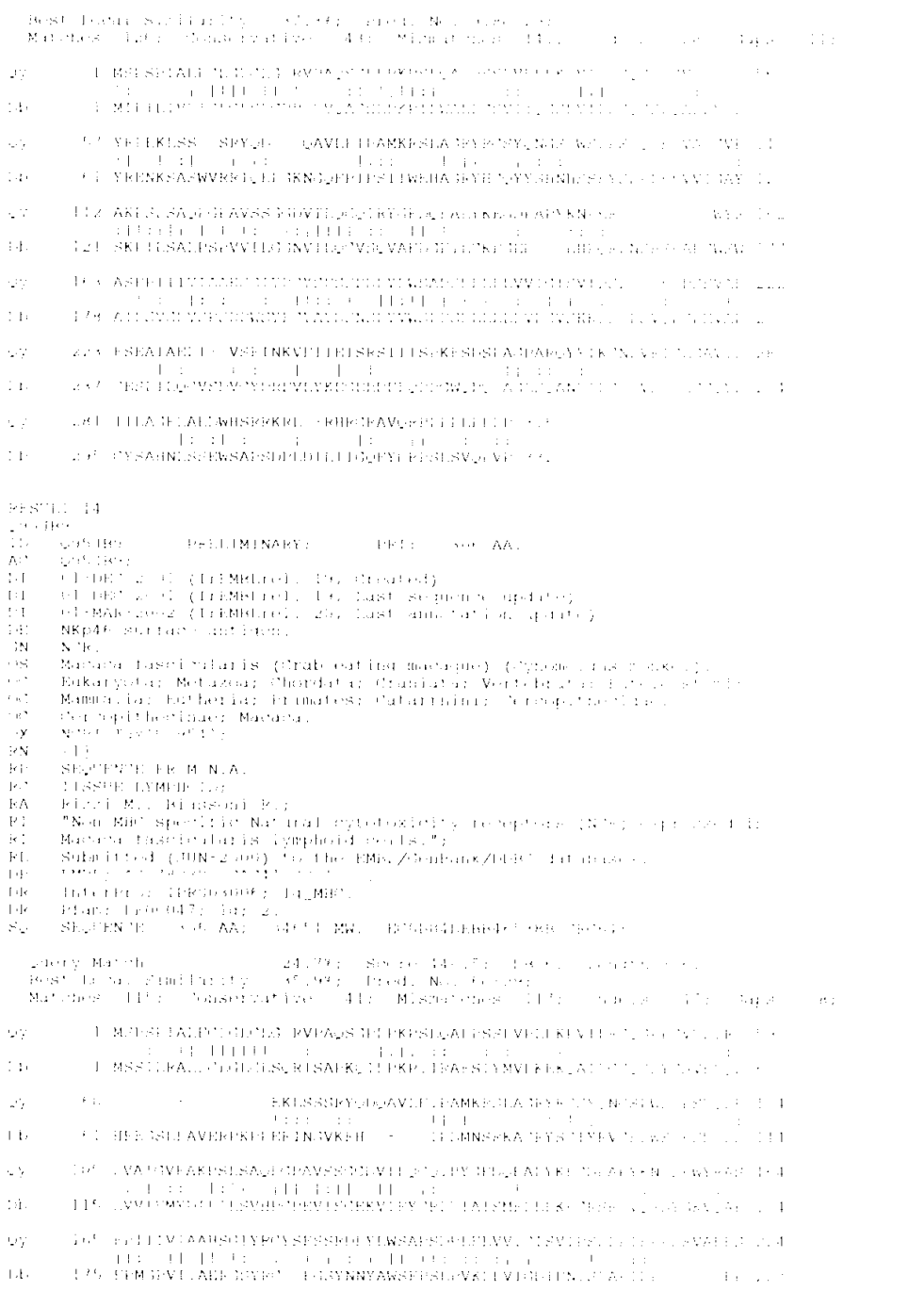












DB protein - protein search, using sw model

Run on: December 5, 2002, 06:54:47 ; Search time 2.0 Seconds
(without alignment)
[illegible] Million cell updates/sec

Title: US-09-503-387-3
Perfect score: 1780
Sequence: 1 MSPSPTALPVGLGLQVEAQSGIEKRSLQALRSSLVE...LKRVIEPSLQ 349

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 844 seqs, 1,241,000 residues

Total number of hits satisfying chosen parameters: 1844

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US60_NEWCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US60_ADDON.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US60_DELETE.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_REVISED.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US60_RESUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US60_CORRECT.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US60_ADDON_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_DELETE_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_REVISED_PUB.pep:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1795	100.8	349	10	US-09-832-512-3	Sequence 3, Appli
2	1782	99.8	349	10	US-09-832-512-64	Sequence 64, Appl
3	1782	99.8	349	10	US-09-832-512-66	Sequence 66, Appl
4	1782	99.8	349	10	US-09-832-512-68	Sequence 68, Appl
5	1782	99.8	349	10	US-09-832-512-70	Sequence 70, Appl
6	1678	94.1	319	10	US-09-832-512-5	Sequence 5, Appli
7	1304	73.0	289	10	US-09-832-512-9	Sequence 9, Appli
8	1122	62.8	313	10	US-09-832-512-10	Sequence 10, Appl
9	1122	62.8	313	10	US-09-832-512-18	Sequence 18, Appl
10	1119	62.6	313	10	US-09-832-512-12	Sequence 12, Appl
11	1119	62.6	313	10	US-09-832-512-41	Sequence 41, Appl
12	1119	62.6	313	10	US-09-832-512-47	Sequence 47, Appl
13	1067.5	60.0	292	10	US-09-832-512-19	Sequence 19, Appl
14	497	27.9	267	10	US-09-832-512-15	Sequence 15, Appl
15	498	27.9	347	9	US-09-870-759-47	Sequence 47, Appl
16	454	25.5	631	10	US-09-832-512-17	Sequence 17, Appl
17	447	25.1	469	10	US-09-841-867-2	Sequence 2, Appl
18	442	24.8	287	10	US-09-832-512-7	Sequence 7, Appl
19	441.5	24.8	416	9	US-09-870-759-48	Sequence 48, Appl
20	426	23.9	1	1	US-09-832-512-2	Sequence 2, Appl
21	408	22.9	37	1	US-09-832-512-3	Sequence 3, Appli
22	227.5	12.7	1	10	US-09-864-761-11	Sequence 11, A
23	226	12.7	37	10	US-09-832-512-2	Sequence 2, Appl
24	224.5	12.6	1	10	US-09-864-761-45	Sequence 45, A
25	224.5	12.6	1	10	US-09-864-761-46	Sequence 46, A
26	224.5	12.6	2	9	US-09-870-759-47	Sequence 47, Appl
27	219.5	12.3	422	10	US-09-925-852-701	Sequence 701, App
28	219	12.3	3	1	US-09-832-512-5	Sequence 5, Appli
29	218.5	12.3	9	10	US-09-864-761-44	Sequence 44, A
30	207	11.6	1	10	US-09-864-761-45	Sequence 45, A
31	202.5	11.4	1	10	US-09-864-761-45	Sequence 45, A
32	193	10.8	1	10	US-09-864-761-44	Sequence 44, A
33	187	10.5	1	1	US-09-832-512-1	Sequence 1, Appl
34	166.5	9.4	80	10	US-09-864-761-48	Sequence 48, A
35	164	9.2	31	10	US-09-832-512-22	Sequence 22, Appl
36	163.5	9.2	269	12	US-10-052-086-544	Sequence 544, App
37	147.5	8.3	459	9	US-09-878-296A-15	Sequence 15, Appl
38	147.5	8.3	459	9	US-09-878-297-45	Sequence 45, Appl
39	147.5	8.3	459	9	US-09-878-192A-45	Sequence 45, Appl
40	144.5	8.1	459	12	US-10-052-086-42	Sequence 42, Appl
41	140.5	7.9	97	10	US-09-864-761-4744	Sequence 4744, A
42	137.5	7.7	97	10	US-09-864-761-4077	Sequence 4077, A
43	136.5	7.7	97	10	US-09-864-761-4,078	Sequence 4156, A
44	136.5	7.7	97	10	US-09-864-761-4178	Sequence 4178, A
45	134.5	7.6	97	10	US-09-864-761-4078	Sequence 4078, A

ALIGNMENTS

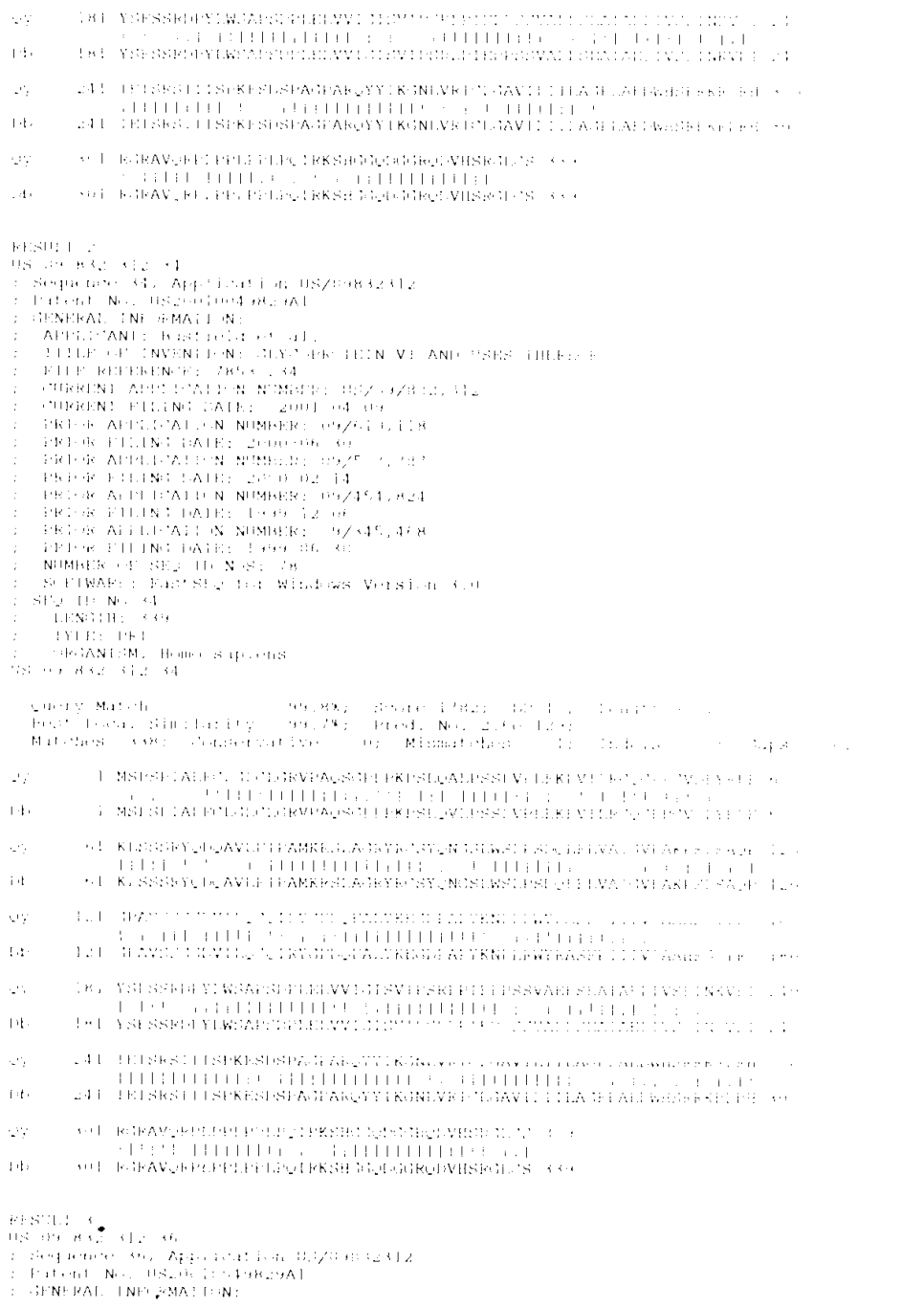
RESULT 1
US-09-832-512-3
; Sequence 3, Application US/09832512
; Publication No. US2002-0164332-A1
; GENERAL INFORMATION:
; APPLICANT: Bustfield et al.
; TITLE OF INVENTION: SEQUENCES VI AND USES THEREOF
; FILE REFERENCE: 7864.264
; CURRENT APPLICATION NUMBER: US/09/832,512
; CURRENT FILING DATE: 2001-04-09
; CLASSIFICATION: 435/69.1
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 09/454,924
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,458
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-512-3

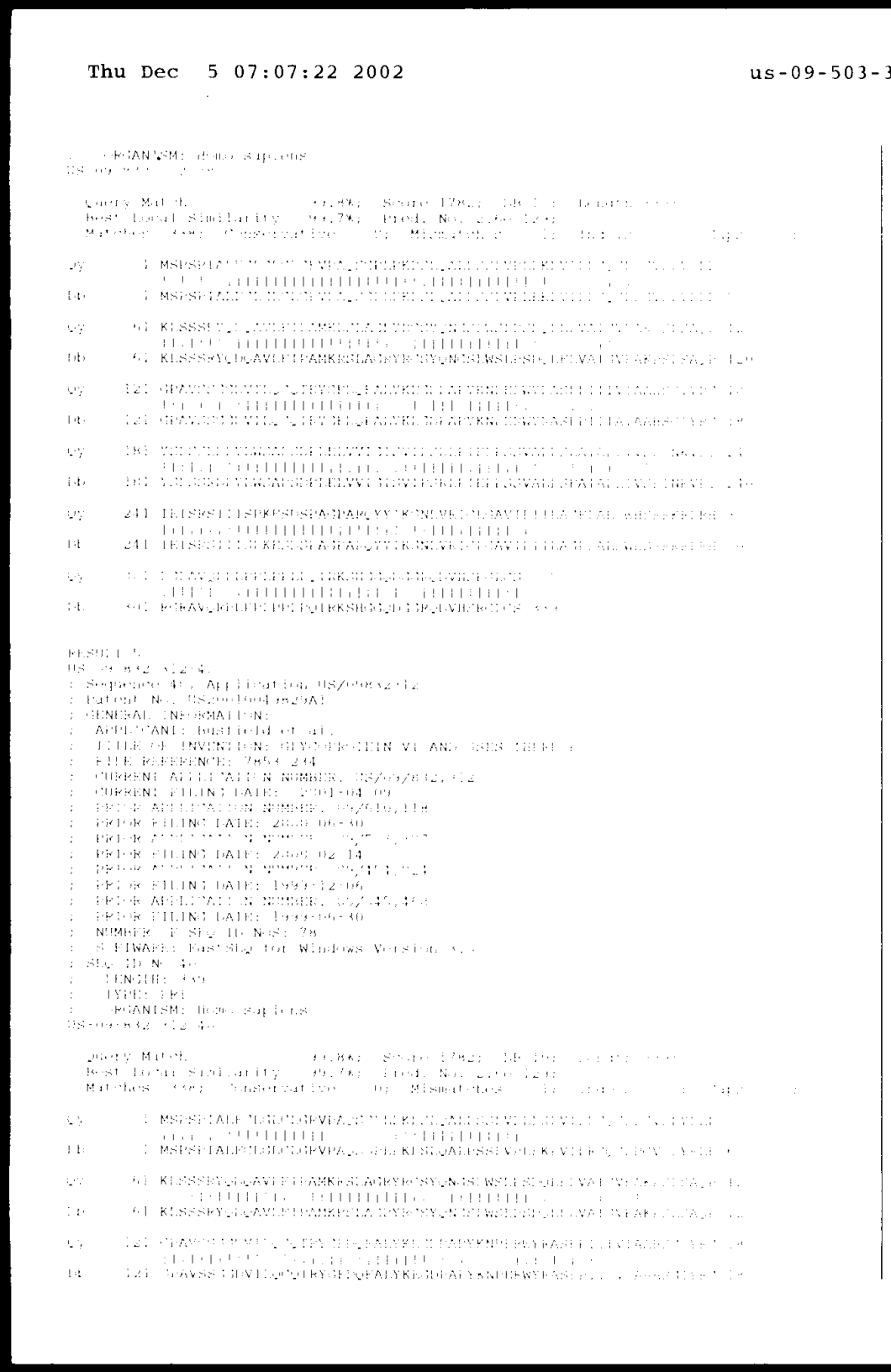
Query Match 100.8%; Score 1795; DB 10; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e-179;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

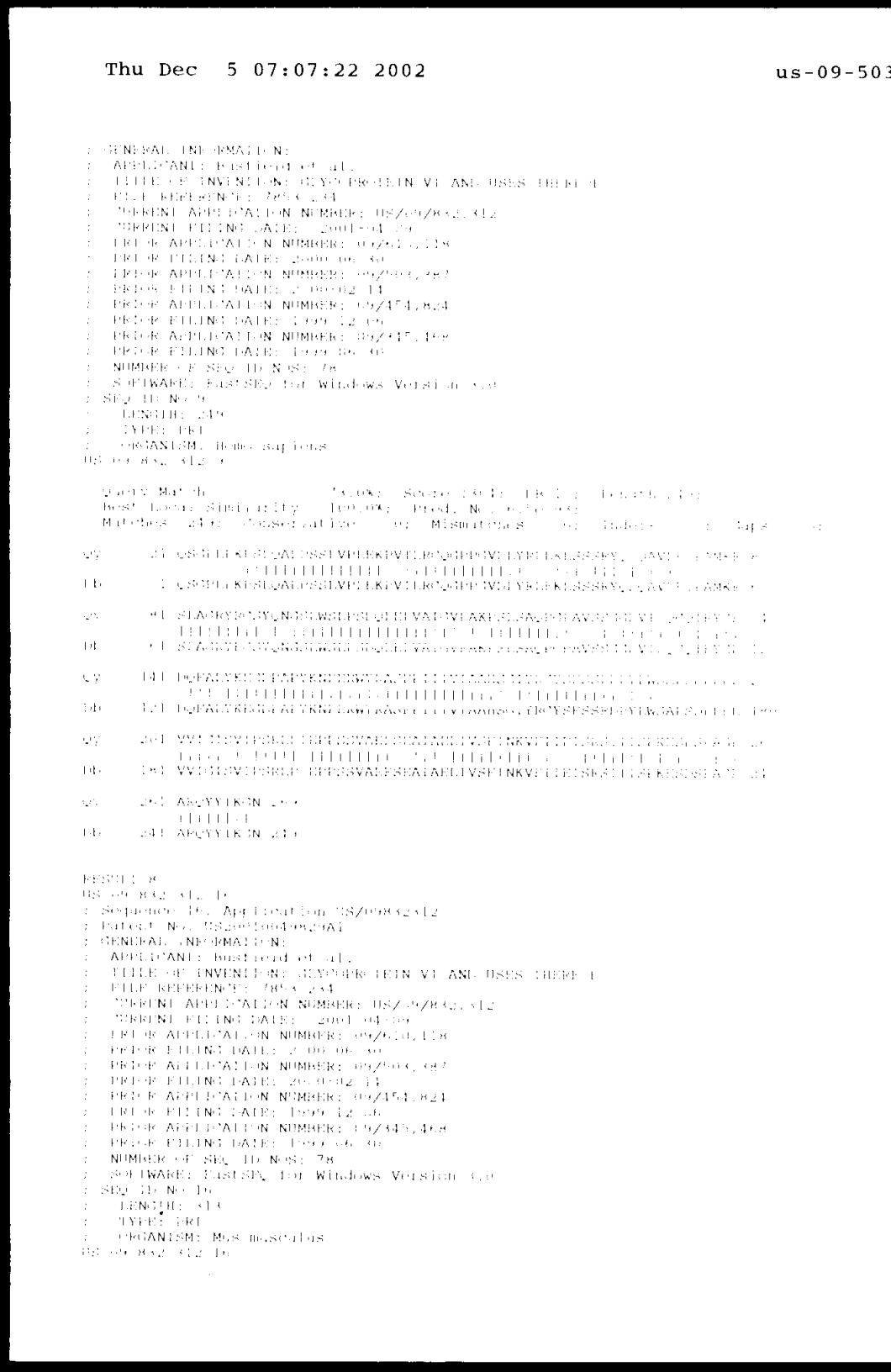
Qy 1 MSPSPTALPVGLGLQVEAQSGIEKRSLQALRSSLVEIKRVIEPSLQDPSPTPPSE 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MSPSPTALPVGLGLQVEAQSGIEKRSLQALRSSLVEIKRVIEPSLQDPSPTPPSE 60

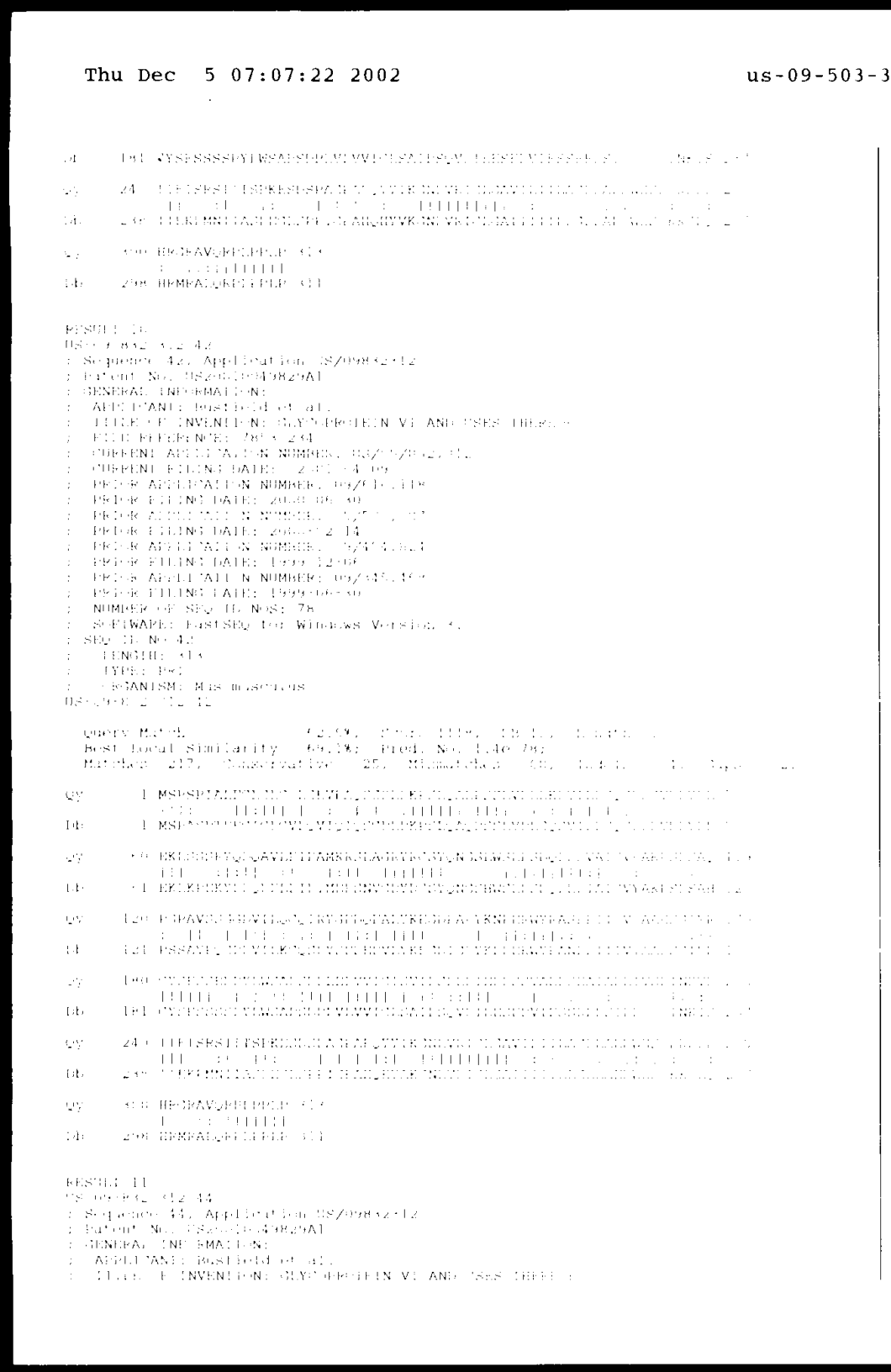
Qy 61 KLSSSSAYQTQAVLHIAMKRSDFSYRCSYQNSSDWSDFSQLELVAIDVEARSRSAQG 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 KLSSSSAYQTQAVLHIAMKRSDFSYRCSYQNSSDWSDFSQLELVAIDVEARSRSAQG 120

Qy 121 QPGVGCVKPCEVSLQLHSDRAGVAIKPPMREGPQSTVMVSIDHCTPMFCQQSEFVFS 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 QPGVGCVKPCEVSLQLHSDRAGVAIKPPMREGPQSTVMVSIDHCTPMFCQQSEFVFS 180









; SEQ ID NO 44
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-503-387-44

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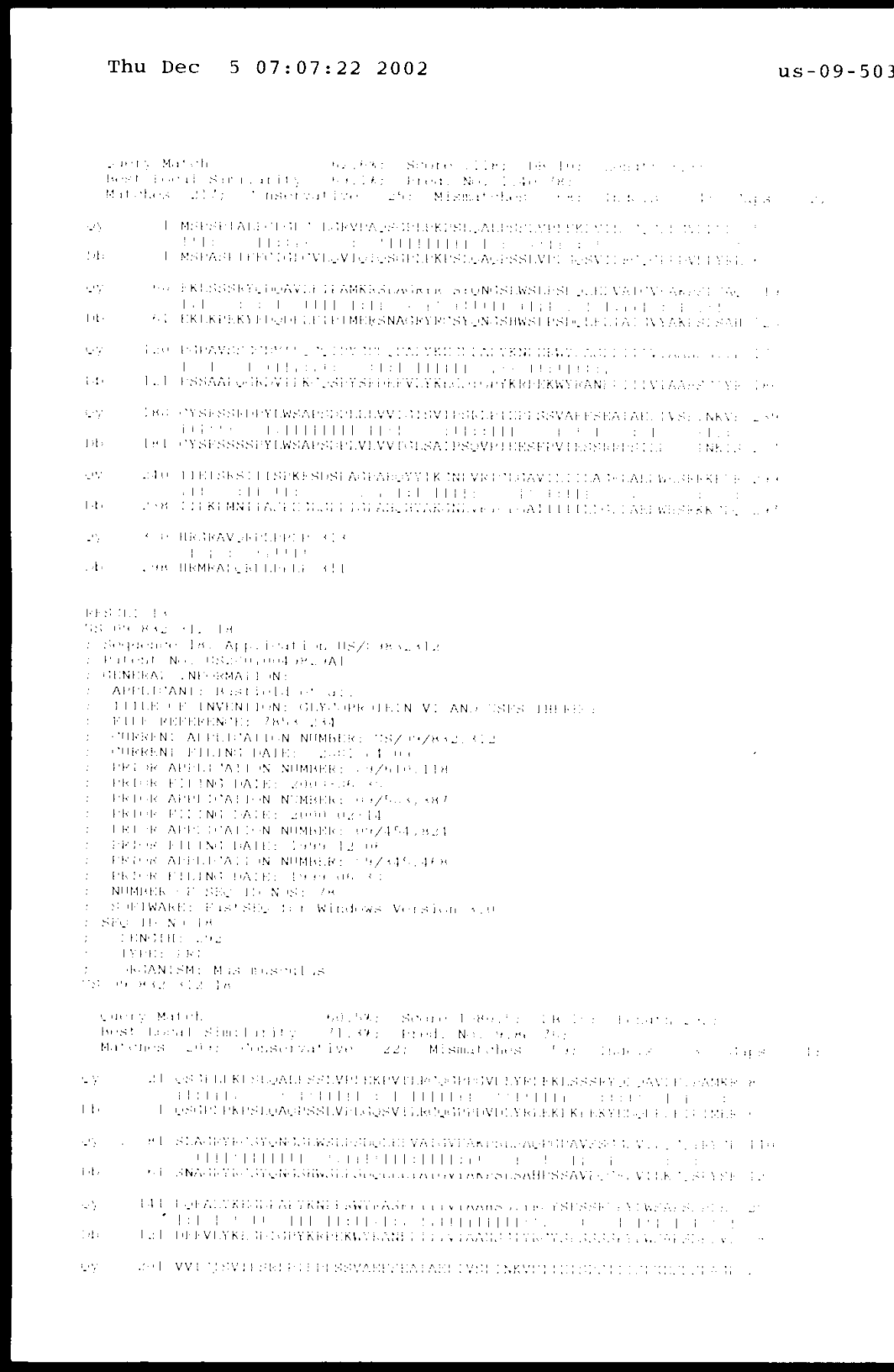
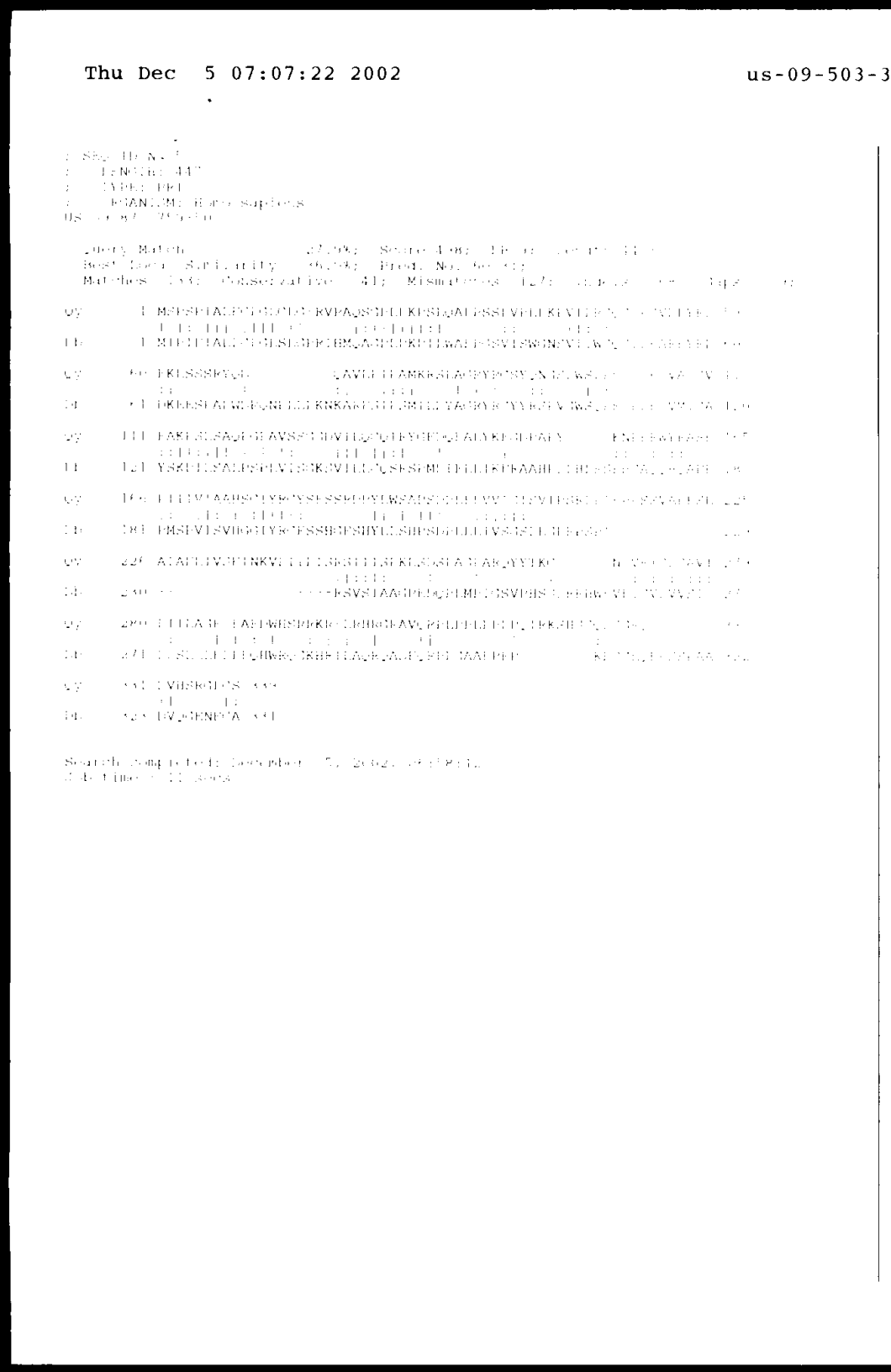
Best Local Similarity 99.3%; Pred. No. 1.4e-206;
Matches 413; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

; SEQ ID NO 45
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-503-387-45

Query Match 99.3%; Score 2114; DB 2; Length 414;
Best Local Similarity 99.3%; Pred. No. 1.4e-206;
Matches 413; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

; SEQ ID NO 46
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-503-387-46





SW protein protein search, using sw model

Run on: December 5, 2002, 06:29:42 ; Search time 2.5 Seconds
(without alignments)
1551.984 Million cell updates/sec

Title: US-09-503-387-3
Perfect score: 4334
Sequence: 1 MEPSEDALYGRQTLSRVIA.....RSSIIQL PSQVIA 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96144422 residues

Word size: 3

Total number of hits satisfying chosen parameters: 566447

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt_96:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

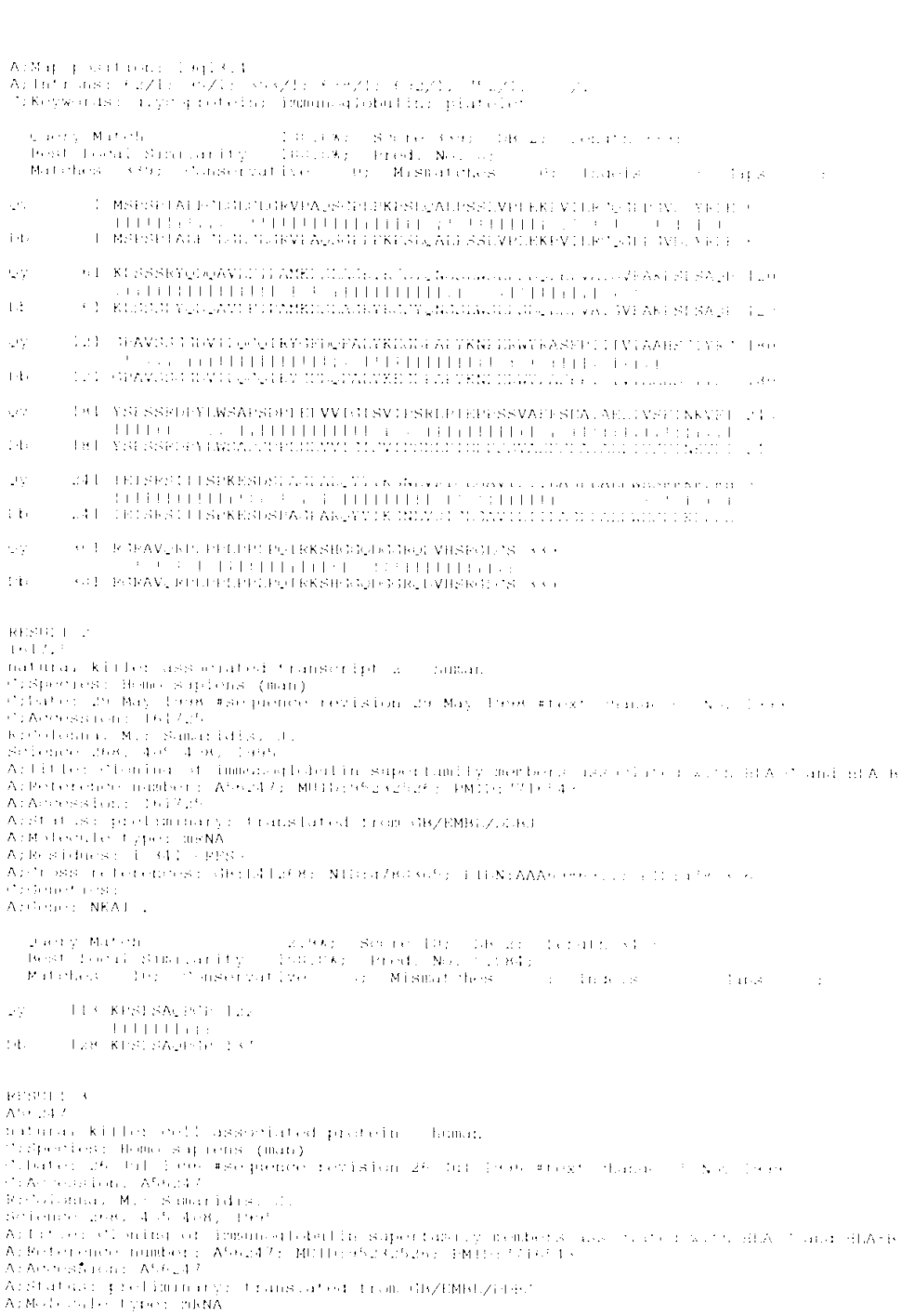
Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4334	100.0	339	2	JC7509	glycoprotein VI l
2	1678	38.7	341	2	I61725	hypothetical prot
3	1	2.9	436	2	AB5247	Sulfate transport
4	1	2.9	427	2	G62484	ankyrin 3, isofo
5	1	2.9	344	2	G81924	KIF1Bbeta2 [imprin
6	1	2.9	144	2	G01925	KIF1Bbeta2 [imprin
7	1	2.9	465	2	G01926	KIF1Bbeta2 [imprin
8	1	2.9	466	2	JC5497	ankyrin 3, isofo
9	1	2.9	535	2	JC5806	kinesin like pro
10	1	2.9	580	2	JC5805	kinesin like pro
11	9	2.7	885	2	A07600	hypothetical prot
12	8	2.4	164	2	I46433	hypothetical prot
13	8	2.4	188	2	B90187	zinc proteinase
14	8	2.4	226	2	I11462	DNA-directed RNA
15	8	2.4	477	2	I46917	hypothetical prot
16	8	2.4	663	1	TVMV88	polyprotein precu
17	8	2.4	1327	2	I09462	DNA-directed RNA
18	8	2.4	2105	2	I10968	transcription fa
19	7	2.1	84	2	B90202	hypothetical prot
20	7	2.1	164	1	B69MZ5	ribosomal protei
21	7	2.1	187	2	G72527	transcription fa
22	7	2.1	253	2	D97438	hypothetical prot
23	7	2.1	255	2	C97020	ribosomal protei
24	7	2.1	266	2	B86972	transcription fa
25	7	2.1	354	2	A47992	116 kDa polypept
26	7	2.1	364	2	S77254	116 kDa polypept
27	7	2.1	370	2	I30459	probable transcr
28	7	2.1	398	2	A60142	hypothetical 16.
29	7	2.1	400	1	B8SB7A	transcription fa
30	7	2.1	401	2	B45488	heat shock protein
31	7	2.1	404	2	AB2465	5'-nucleotidase
32	7	2.1	414	2	I48434	ankyrin type II
33	7	2.1	438	2	S44288	probable transmem
34	7	2.1	439	2	I30463	probable F-actin
35	7	2.1	451	2	B62574	Na,K-transporting
36	7	2.1	454	2	S47917	probable membrane
37	7	2.1	455	2	A72468	ankyrin type II
38	7	2.1	456	2	I47755	116 kDa type II
39	7	2.1	461	2	I49925	probable nucleot
40	7	2.1	464	2	S74450	hypothetical pro
41	7	2.1	484	2	T50481	hypothetical pro
42	7	2.1	485	2	I45113	ankyrin type II
43	7	2.1	500	2	I34089	hypothetical pro
44	7	2.1	504	2	I42580	ketoacyl-ACP syn
45	7	2.1	545	2	I47851	hypothetical pro
46	7	2.1	554	2	I46023	ribosomal protei
47	7	2.1	554	2	A72469	ribosomal protei
48	7	2.1	554	2	S43588	ribosomal protei
49	7	2.1	575	2	T50420	lipase related p
50	7	2.1	585	2	I49512	ankyrin type II
51	7	2.1	594	2	B49356	dihydroorotate d
52	7	2.1	597	2	T46452	DnaA protein hom
53	7	2.1	607	2	A64787	hypothetical pro
54	7	2.1	608	2	C64536	probable transcr
55	7	2.1	610	2	C70869	transcription re
56	7	2.1	611	2	A12451	transcription re
57	7	2.1	615	2	B70878	hypothetical pro
58	7	2.1	620	2	A61084	phosphoglycerate
59	7	2.1	620	2	A12441	phosphoglycerate
60	7	2.1	622	2	B70547	probable transcr
61	7	2.1	622	2	A12725	transcription re
62	7	2.1	624	2	A72894	hypothetical pro
63	7	2.1	630	1	KBBYTh	cytochrome P-450
64	7	2.1	630	2	I55505	hypothetical prot
65	7	2.1	638	2	S60888	protein B4954.1
66	7	2.1	640	2	S75408	probable oxidored
67	7	2.1	640	2	A12600	ribosomal protein
68	7	2.1	651	2	JC7712	hypothetical prot
69	7	2.1	655	2	A62852	transcription reg
70	7	2.1	660	2	A00629	hypothetical prot
71	7	2.1	664	2	B67669	cell-peptide ABC
72	7	2.1	670	2	C48846	hypothetical prot
73	7	2.1	671	2	S47383	hypothetical prot
74	7	2.1	675	2	B64965	ribosomal protein
75	7	2.1	683	2	AE2437	hypothetical pr

ALIGNMENTS

RESULT 1
JC7509
glycoprotein VI l - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #tree_grafting 07-Jun-2002
C;Accession: JC7509; JC721
R;Ezumi, Y.; Ohbayama, T.; Takeda, H.
Biochem. Biophys. Res. Commun. 278, 27-36, 2000
A;Title: Molecular cloning, genetic structure, chromosomal localization, and alternat
A;Reference number: JC7509; MUID:21048673; PMID:11027644
A;Contents: platelet
A;Accession: JC7509
A;Molecule type: mRNA
A;Residues: 1-339 <EZU>
A;Cross-references: UniProt:Q9HCN8
A;Accession: JC7101
A;Molecule type: protein
A;Residues: 28-41;62-79;131-142 <EZU>
C;Comment: This protein, which belongs to the immunoglobulin superfamily, is the majo
of platelet collagen receptor, mediates platelet adhesion, and plays some roles in cell
C;Genetics:
A;Gene: GpVI



RESULT 6
Qy 1 ... 22
Db 22 ... 22

RESULT 7
Qy 1 ... 22
Db 22 ... 22

RESULT 8
Qy 1 ... 22
Db 22 ... 22

RESULT 9
Qy 1 ... 22
Db 22 ... 22

RESULT 10
Qy 1 ... 22
Db 22 ... 22

```
A;Cross references: GB:AF541165; NID:g27818501; PID:AAO64...; ...
C;Comment: This protein functions as inhibitory cell surface ... cell ...
C;Genetics:
A;Map position: 7
F;1-23/Domain: signal sequence #status predicted
F;24-118,119-220,221-315,316-418,419-517,518-616/Domain: ... #status p
F;536-574/Domain: transmembrane #status predicted
F;575-600/Domain: cytoplasmic #status predicted

  Query Match              2.9%;  Score 19;  DB 2;  Length ...;
  Best Local Similarity   100.0%;  Pred. No. ...;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PPSPLELVVP 10
          ||||||||||
Db    120 PPSPLELVVP 129


RESULT 11
S62000
hypothetical protein YEL111w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L9275
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change ...
C;Accession: S62000
R;Proper, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.; Wilmen, A.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S62000
A;Accession: S62000
A;Molecule type: DNA
A;Residues: 1-805 <EIE>
A;Cross references: EMBL:Z24105; NID:g145111...; ...
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:YEL111w
A;Cross references: SGD:S0000...
A;Map position: 5

  Query Match              2.7%;  Score 18;  DB 2;  Length ...;
  Best Local Similarity   100.0%;  Pred. No. ...;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      506 PLPPLPPLPP 515
          ||||||||||
Db      193 PLPPLPPLPP 202


RESULT 12
146433
hypothetical protein DKFZp434E0326.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Jan-2...
C;Accession: 146433
R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhauer, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z20038
A;Accession: 146433
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <AAA>
A;Cross references: EMBL:AL137463
A;Experimental source: adult testis; clone DKFZp434E0326
C;Genetics:
A;Note: DKFZp434E0326.1

  Query Match              2.4%;  Score 8;  DB 2;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. ...;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      174 PSDETEIV 181
          ||||||||
Db       88 PSDETEIV 95


RESULT 13
P40180
CYB protein - Synechococcus sp. (strain PCC 7942) (fragment)
C;Species: Synechococcus sp.
C;Date: 01-Dec-1991 #sequence_revision 01-Dec-1991 #text_change 16-Jan-2...
C;Accession: P40180
R;Lundenbach, D.E.; Berbert, S.K.; Medewell, C.; Berk, D.; Grossman, A.R., ...
Plant Cell 2, 915-924, 1990
A;Title: Cytochrome c-555 is not required for photosynthetic activity in the Synecho...
A;Reference number: P40180; MUID:91068...; PMID:19...
A;Accession: P40180
A;Molecule type: DNA
A;Residues: 1-186 <LAU>
C;Genetics:
A;Gene: CYB
C;Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat
F;92-125/Domain: tetratricopeptide repeat homology <TTR>
F;126-159/Domain: tetratricopeptide repeat homology <TTR>

  Query Match              2.4%;  Score 8;  DB 2;  Length 186;
  Best Local Similarity   100.0%;  Pred. No. ...;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      178 AQLCPAVS 185
          ||||||||
Db      179 AQLCPAVS 186


RESULT 14
I37452
cytochrome-c oxidase (EC 1.9.3.1) chain II - Sphaerodactylus roosevelti mitochondrion
C;Species: mitochondrion Sphaerodactylus roosevelti
C;Date: 15-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 23-Jan-2...
C;Accession: I37452
R;Crease, T.J.
Gene 233, 89-98, 1999
A;Title: The complete sequence of the mitochondrial genome of Sphaerodactylus roosev...
A;Reference number: Z27264; MUID:99...; PMID:10...
A;Accession: I37452
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-227 <CRE>
A;Cross references: EMBL:AF117817; NID:g4...; PID:g4...; PID:AAD...
C;Genetics:
A;Gene: COII
A;Gene: mitochondrion
A;Genetic code: SGC4
C;Superfamily: cytochrome c oxidase chain II; cytochrome c oxidase chain II homolog
C;Keywords: copper; electron transfer; membrane-associated complex; mitochondrial inn
F;9-214/Domain: cytochrome-c oxidase chain II homology <Cyt>
F;161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted
F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted
F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

  Query Match              2.4%;  Score 8;  DB 2;  Length 227;
  Best Local Similarity   ...%;  Pred. No. ...;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      277 AVILILLA 284
          ||||||||
Db       70 AVILILLA 77


RESULT 15
AAH67...
hypothetical protein DKFZp779K1647.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2005 #sequence_revision 17-Mar-2005 #text_change 17-Mar-2...
C;Accession: AAH67...
R;Strausberg, R.; Feingold, E.; Grouse, L.; Derge, J.; Klausner, R.; Collins, F.; Wagner, L.; ...
submitted to the Protein Sequence Database, February 2005
A;Reference number: Z24...
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A;Accession: [illegible]
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-477 <AAA>
A;Cross-references: EMBL:AL[illegible]
A;Experimental source: natural melatonin (MeW: [illegible]
C;Genetics:
A;Note: GK=2p[illegible]

Query Match [illegible]; Score 8; DB 2; Length [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

Qy [illegible]
[illegible]
Db [illegible]

RESULT 16
[illegible]
protein tyrosine kinase (EC [illegible]) fr[illegible]
C;Species: Rous sarcoma virus
A;Note: src1 Bolis sp. (rat)
C;Date: 27-Nov-1985 #sequence_revision 26-May-1987 #text_change [illegible]
C;Accession: A00655; A03947
R;Nakamura, S.; Kobatake, K.; Reddy, E.P.
Science 228, 1096-, 1984
A;Title: Gene product of v-fps oncogene hybrid protein contains [illegible]
A;Reference number: A00655; MUID:84287742; PMID:[illegible]
A;Accession: A00655
A;Molecule type: DNA
A;Residues: 1-663 <NAH>
A;Cross-references: GB:X00265; GB:Kol1987; NID:g[illegible]; [illegible]
A;Note: the authors translated the codon GAT for residue 1 as [illegible]
C;Comment: This protein is synthesized as a dead [illegible]
C;Genetics:
A;Gene: fps
C;Superfamily: feline sarcoma virus protein tyrosine kinase [illegible]
C;Keywords: ATP; [illegible]phosphorylation; [illegible]
F;1-11/Region: [illegible]
F;141-268/Region: [illegible]
F;228-[illegible]
F;[illegible]
F;413/Region: protein kinase ATP binding [illegible]
F;452/Active site: lys #status predicted

Query Match [illegible]; Score 8; DB 1; Length [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible]
[illegible]

Qy [illegible]

Db [illegible]

RESULT 17
[illegible]
immunoglobulin-like protein [NSFL] human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision [illegible] #text_change [illegible]
C;Accession: I49102
R;Mazzarella, R.; Petaja, G.; Jones, D.; Jones, C.; SCL [illegible]
Genomics 48, 257-262, 1998
A;Title: Cloning and expression of an immunoglobulin-[illegible] (IGSF1) in Xq25
A;Reference number: Z11663; MUID:98190514; PMID:[illegible]
A;Accession: I49102
A;Status: preliminary; translated to [illegible]
A;Molecule type: mRNA
A;Residues: 1-527 <MAZ>
A;Cross-references: EMBL:AF[illegible]; NID:g[illegible]
C;Genetics:
A;Gene: IGSF1
A;Map position: Xq2[illegible]

Query Match [illegible]; Score 8; DB 2; Length [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

Qy 194 PSDFLELV 201
[illegible]
Db 1251 PSCPGELV 1258

RESULT 18
I18968
protable serine-type carboxypeptidase (EC 3.4.16.-) Y1684A.2 - [illegible] stabilis [illegible]
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change [illegible]
C;Accession: I18968; I24145; I26477
R;Thomas, K.
Submitted to the EMBL Data Library, March 1996
A;Reference number: Z19654
A;Accession: I18968
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2105 <WIL>
A;Cross-references: EMBL:Z[illegible]; [illegible]
A;Experimental source: clone [illegible]
R;Lloyd, C.
Submitted to the EMBL Data Library, March 1997
A;Reference number: Z19697
A;Accession: I24145
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2105 <WIL>
A;Cross-references: EMBL:Z[illegible]; [illegible]
A;Experimental source: clone [illegible]
R;Wallis, J.
Submitted to the EMBL Data Library, June 1998
A;Reference number: Z20222
A;Accession: I26477
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2105 <WIL>
A;Cross-references: [illegible]
A;Experimental source: clone Y1684A
C;Comment: This protein has 4 repeats of sequence homology to serine carboxypeptid
C;Genetics:
A;Gene: CESP:Y1684A.2
A;Map position: X
[illegible]
C;Keywords: duplication; hydrolase; serine carboxypeptidase

Query Match [illegible]; Score 8; DB 2; Length 2105;
Best Local Similarity [illegible]; Pred. No. 4[illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy 909 LPFLPPFLP 916
[illegible]
Db 975 LPFLPPFLP 982

RESULT 19
E69268
Hypothetical protein AF034 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: E69268
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
; Dodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Sterholz, I.; [illegible] M.; Spelzes, T.; Attlach, T.; Kaiser, P.; Sykes,
Smith, H.; Weeser, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing ar

```
A;Reference number: A<sup>[illegible]</sup>; MEDLINE:[illegible]; PMID:[illegible]
A;Accession: [illegible]
A;Title: preliminary nucleic acid sequence no. [illegible]
A;Molecule type: DNA
A;Residues: 1 bp  KUK>
A;Cross-references: GB:AE[illegible]; GB:AE[illegible]; NID:[illegible]; N:AAA[illegible]; PID:g[illegible]

  Query Match              2.1%;  Score 7;  DB 2;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. 2%;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      [illegible] CCCAATC 208
              |||||||
Db      [illegible] CCCAATC 98


RESULT 20
P[illegible]
ribosomal protein PSCL25 precursor, chloroplast  [imported]
C;Species: Lycopersicon esculentum (garden pea)
C;Date: 31-Mar-[illegible] #sequence_revision 31-Mar-[illegible] #text_change [illegible]
C;Accession: S04[illegible]
R;Gantt, J.S.
Plant Mol. Biol. 14, 565-568, 1990
A;Title: Nucleotide sequences of tRNAs encoding [illegible] chloroplast [illegible]
A;Reference number: S[illegible]; MEDLINE[illegible]; PMID[illegible]
A;Accession: S04[illegible]
A;Molecule type: mRNA
A;Residues: 1-104 <GAN>
A;Cross-references: EMBL:X[illegible]; NID:g[illegible]; PID:[illegible]
C;Superfamily: pea chloroplast ribosomal protein PSCL25
C;Keywords: chloroplast; protein biosynthesis; ribosome
F;1-[illegible]/Domain: transit peptide (chloroplast) #status predicted
F;[illegible]/Product: ribosomal protein PSCL25 #status predicted MAT

  Query Match              2.1%;  Score 7;  DB 1;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches    2;  Conservative    0;  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy      [illegible] TTTGTGC 234
              |||||||
Db      [illegible] TTTGTGC [illegible]


RESULT 21
S72[illegible]
hypothetical protein APE2126 - Aeropyrum pernix (strain K)
C;Species: Aeropyrum pernix
C;Date: 26-Aug-[illegible] #sequence_revision 26-Aug-[illegible] #text_change [illegible]
C;Accession: S72[illegible]
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Ikuo, K.; Sa
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aerop
A;Reference number: A72[illegible]; MEDLINE[illegible]; PMID[illegible]
A;Accession: S72[illegible]
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-127 <KAW>
A;Cross-references: GB:AP[illegible]; NID:g[illegible]; PID:g[illegible]; PID:g[illegible]
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE2126
C;Superfamily: Aeropyrum pernix hypothetical protein APE2126

  Query Match              2.1%;  Score 7;  DB 2;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. 2%;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      [illegible] ISVIDSG 211
              | | |||
Db      [illegible] ISVIDSG [illegible]


RESULT 22
P[illegible]
hypothetical protein SMa1156 [imported] - Sinorhizobium meliloti (strain [illegible]) [illegible]
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change [illegible]
C;Accession: P[illegible]
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.Y.; Barloy-Hubler, F.; B
.; Kalman, S.; Kaufman, R.W.; Kathir, P.; Luck, M.; Margolski, D.; Wong, K.; Yelto, K
Sci. U.S.A. 98, [illegible], 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
A;Reference number: A[illegible]; MUID:[illegible]; PMID:[illegible]
A;Accession: P[illegible]
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-[illegible] <KUK>
A;Cross-references: GB:AE[illegible]; NID:[illegible]; PID:[illegible]; GSDB:[illegible]
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
J.; Berry, A.M.; Bruhn, D.F.; Dusha, K.; Fisher, R.F.; Flores, S.; Ford, T.; Gallon,
S.; Hyman, R.W.; Jones, J.
Science 293, 668-672, 2001
A;Authors: Kuhn, D.; Kuhn, M.L.; Kaiman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelo,
Mehandi, P.; Vandenbosch, M.; Vorhoelter, F.J.; Weidner, S.; Wells, G.B.; Ward, K.; Yel
A;Title: The complete genome of the legume symbiont Sinorhizobium meliloti
A;Reference number: A[illegible]; MUID:[illegible]; PMID:[illegible]
A;Contents: annotation
C;Genetics:
A;Gene: SMa1156
A;Genome: plasmid

  Query Match              2.1%;  Score 7;  DB 2;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. 44;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      245 KSIIISP 251
              |||||||
Db      134 KSIIISP 140


RESULT 23
[illegible]
riboflavin synthase, beta chain [imported] - Streptococcus pneumoniae (strain [illegible])
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: C[illegible]
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; N
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapp
nson, D.; Hickey, E.K.; Bolt, I.E.
Science 293, 498-506, 2001
A;Authors: Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A[illegible]; MUID:[illegible]; PMID:[illegible]
A;Accession: C[illegible]
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-[illegible] <KUK>
A;Cross-references: GB:AE[illegible]; NID:g[illegible]; PID:g[illegible]; GSDB:[illegible]
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0[illegible]
C;Superfamily: riboflavin synthase beta chain

  Query Match              2.1%;  Score 7;  DB 2;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. 44;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      [illegible] IEIGAVI 279
              | | |||
Db      [illegible] IEIGAVI 82


RESULT 24
```

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RESULT 24
B96972
riboflavin synthase beta chain (imported) - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2002 #sequence_revision 14-Sep-2002 #text_change 14-Sep-2002
C;Accession: B96972
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Makarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.; Birren, B.; Fraser, C.; Koonin, E.V.; Smeianov, V.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21454626; PMID:21454627
A;Accession: B96972
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <KOR>
A;Cross-references: GB:AE001437; NID:g15894978; PIDN:AAK79971.1; PID:g15894979
A;Experimental source: Clostridium acetobutylicum; ATCC 824
C;Genetics:
A;Gene: CAC0533
C;Superfamily: riboflavin synthase beta chain

  Query Match 2.1%; Score 7; DB 2; Length 159;
  Best Local Similarity 33.3%; Pred. No. 44;
  Matches 7; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 273 DCIGAVI 279
          |:|||||
Db 76 DCIGAVI 82


RESULT 25
A97892
riboflavin synthase (EC 2.5.1.9) beta chain [imported] - Streptococcus pneumoniae (strai
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 16-Nov-2001
C;Accession: A97892
R;Hakenbeck, J.S.; Ait-Ze, W.; Arnold, J.; Blueschke, U.; Fuchs, K.; Gilles, A.F.; Gi
e, R.; Hoskins, J.; Lee, L.N.; Leiknes, E.J.; Lu, T.; Matsushita, M.; McAllen, S.; M
y, P.; Sun, P.M.; Wirkley, M.E.
J. Bacteriol. 183, 6709-6717, 2001
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain Rx
A;Reference number: A97892; MUID:21422345; PMID:21544...4
A;Accession: A97892
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-155 <KOR>
A;Cross-references: GB:AE007317; NID:g15902...; PIDN:AAK...; PID:g15902...
C;Genetics:
A;Gene: ribE
C;Superfamily: riboflavin synthase beta chain
C;Keywords: transferase

  Query Match 2.1%; Score 7; DB 2; Length ...;
  Best Local Similarity 100.0%; Pred. No. 44;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 DCIGAVI 279
          |||||||
Db 76 DCIGAVI 82


RESULT 26
S77244
riboflavin synthase (EC 2.5.1.9) beta chain - Synechocystis sp. (strain PCC 6803)
N;Alternate names: 6,7-dimethyl-8-ribityllumazine synthase [incorporated]
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 26-Apr-1997 #sequence_revision 26-Apr-1997 #text_change ...-...-...
C;Accession: S77244
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, ...; Nakajima, N.;
o, K.; Kohara, M.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
```

```
S.
A;Reference number: S74322; MUID:97016201; PMID:8905231
A;Accession: S77244
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-164 <KAN>
A;Cross-references: EMBL:dbj|D90912; NID:g1652116; PIDN:BAA15067.1; PID:g1652117
A;Note: the nucleotide sequence was submitted to the EMBL data library, July 1996
C;Genetics:
A;Gene: ribH
C;Function:
A;Pathway: riboflavin biosynthesis
C;Superfamily: riboflavin synthase beta chain
C;Keywords: flavoprotein; riboflavin biosynthesis; transferase
F;94/active site: His #status predicted

  Query Match ...%; Score 7; DB 2; Length 164;
  Best Local Similarity ...%; Pred. No. 47;
  Matches 7; Conservative ... Mismatches ...; Indels ...; Gaps ...;

Qy 273 DCIGAVI 279
          |||||||
Db 82 DCIGAVI 88


RESULT 27
F70920
probable acetyltransferase - Mycobacterium tuberculosis (strain H37Rv)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change ...-...-200...
C;Accession: F70920
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Eiglmeier, K.; Gas, S.; Barry, C.E. 3rd; Tekaia, F.; Badcock, K.; Basham, D.; Brown,
Barrell, B.G.
Nature 393, 537-544, 1998
A;Authors: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom
A;Reference number: A70500; MUID:98259897; PMID:9634230
A;Accession: F70920
A;Status: preliminary; not translated; from 1 publication
A;Molecule type: DNA
A;Residues: 1-170 <COL>
A;Cross-references: GB:Z77163; GB:AL...; NID:g...; PIDN:CAB...; PID:g...
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: moaC
C;Superfamily: molybdenum cofactor biosynthesis protein C

  Query Match ...%; Score 7; DB 2; Length ...;
  Best Local Similarity 100.0%; Pred. No. 48;
  Matches 7; Conservative ... Mismatches ...; Indels ...; Gaps ...;

Qy 41 EKIVILM 47
          :|||||
Db 24 EKIVILM 30


RESULT 28
A80152
conserved hypothetical protein YE1174 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-200...
C;Accession: A80152
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M
deno Iarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, ...
il, M.; Rutherford, K.; Simmonds, M.; Skelton, ...; Stevens, K.; Whitehead, S.; Barre
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: A80001; MUID:...; PMID:11586360
A;Accession: A80152
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-188 <KUR>
```

A;Cross-references: GB:AL590084.1; EMBL:CAB50884.1; NP_416277.1; GI:16129720;
C;Genetics:
A;Gene: Yi 1074
C;Superfamily: cspA protein

Query Match 2.1%; Score 7; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 219 SVALESF 225
||||||
Db 96 SVALESF 102

RESULT 29
B65388
beef shock protein dnaJ - Caldanaerobacter crossenii (fragment)
C;Species: Caldanaerobacter crossenii
C;Date: 31-Aug-1998 #sequence_revision 31-Aug-1998 #text_change 27-Aug-2002
C;Accession: B65388
R;Gomez, S.L.; Gebert, J.W.; Shapiro, L.
J. Bacteriol. 172, 3051-3059, 1990
A;Title: Expression of the Caulobacter heat shock gene dnaK is developmentally contro
A;Reference number: A65388; MUID:90274207; PMID:2341141
A;Accession: B65388
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <GOM>
A;Cross-references: GB:M55224; NID:g144221; PIDN:AAA24724.1; PID:g144222; GB:M57667
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino terminal homology
C;Keywords: DNA replication; heat shock; molecular chaperone
F;3-66/Domain: dnaJ amino-terminal homology <DNJ>
F;75-129/Region: G/F motif
F;147-154/Region: CAAGAAG repeat
F;154-171/Region: AAGAAG repeat

Query Match 2.1%; Score 7; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 GRAVQKP 86
|||||||
Db 138 GRAVQKP 144

RESULT 31
A82405
2,7 didethyl 8 ribityllumazine synthase (riboflavin synthase beta chain) (EC 2.5.1.9) [imported]
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 28-Jun-2002
C;Accession: AB2405
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriya
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Kohara, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB2405; MUID:21595285; PMID:11759840
A;Accession: AB2405
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-150 <KUR>
A;Cross-references: GB:BA000020; PIDN:BAB72702.1; PID:g17131120; GSPDB:GN00176
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all3993
C;Superfamily: riboflavin synthase beta chain

Query Match 2.1%; Score 7; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 DTGAVI 279
||||||
Db 81 DTGAVI 87

RESULT 32
[illegible]
conserved hypothetical protein SMb20679 [imported] [illegible] (strain 1021
C;Species: Sinorhizobium meliloti
C;Date: 24-Apr-2001 #sequence_revision 24-Apr-2001 #text_change 16-Jul-2001
C;Accession: [illegible]
R;Glaser, P.; Weidner, S.; Wehmeier, K.; Bahrmann, G.; Thierbach, G.; Hermann
Proc. Natl. Acad. Sci. U.S.A. 98, 9358-9363, 2001
A;Title: The complete sequence of the 1,683 kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A96042; MUID:21265566; PMID:11504915
A;Accession: B96042
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1391 <KUR>
A;Cross-references: GB:AL591985; PID:CAC47742.1; pid:[illegible]; GSDB:SN
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Covitz, R.J.; Davis, R.W.; Dreano, S.; Fuhrmann, A.; Gouzy, J.; Ma
Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wu, Y.; Yeng, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti
A;Reference number: A96049; MUID:21368234; PMID:11431563
A;Contents: annotation
C;Genetics:
A;Gene: SMb20679
A;Genome: plasmid

Query Match 2.1%; Score 7; DB 2; Length [illegible]
Best Local Similarity [illegible]%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 AFSAPLE 199
[illegible]
Db 117 AFSDPLE 123

RESULT 33
Q82576
probable transcription regulator PA2885 [imported] [illegible] (strain PA
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 16-Jul-2001
C;Accession: Q82576
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
adman, S.J.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
J.; Loty, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa [illegible] opportunistic patha
A;Reference number: A82576; MUID:20417717; PMID:10984043
A;Accession: Q82576
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-198 <SIO>
A;Cross-references: GB:AE004711; GB:AE004091; NID:g9951211; PID:AAG08429.1; GSDB:SN
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: [illegible]

Query Match 2.1%; Score 7; DB 2; Length [illegible]
Best Local Similarity [illegible]%; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy 193 LELVAPE 199
[illegible]
Db 2 LELVAPE 8

RESULT 34
D96024
probable C-P (carbon-phosphorus) lyase complex protein [imported] [illegible] Sinorhizobium meli
C;Species: Sinorhizobium meliloti
C;Date: 24-Apr-2001 #sequence_revision 24-Apr-2001 #text_change 16-Jul-2001

C;Accession: D96024
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683 kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A96042; MUID:21265566; PMID:11504915
A;Accession: D96024
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-200 <KUR>
A;Cross-references: GB:AL591985; PID:CAC47742.1; pid:[illegible]; GSDB:SN
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Covitz, R.J.; Davis, R.W.; Dreano, S.; Fuhrmann, A.; Gouzy, J.; Ma
Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wu, Y.; Yeng, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti
A;Reference number: A96049; MUID:21368234; PMID:11431563
A;Contents: annotation
C;Genetics:
A;Gene: phdE; SMb20760
A;Genome: plasmid

Query Match 2.1%; Score 7; DB 2; Length 200
Best Local Similarity [illegible]%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 189 GIEqPAL 195
[illegible]
Db 110 GFEqPAL 116

RESULT 35
Q82578
CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase XF2410 [imported]
C;Species: Xylella fastidiosa
C;Date: 16-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 16-Jul-2001
C;Accession: Q82578
R;Simpson, A.J.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
as Neto, E.; Dockena, C.; Ferro, E.S.; Ferro, J.A.; Ferro, M.I.T.; Ferro, M.I.; Fr
Gruber, A.; Hagler, A.N.; Jorge, J.A.; Kitajima, J.P.; Kobargi, R.; Kuramae, E.E.; La
Leite, R.P.; Lemos, E.G.; Lemos, M.V.F.; Lopes, C.R.; Machado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Monteiro-Vitorello, C.B.; Moon, D.H.; Nagai, M.A.; Nascimento, A.L.T.O.; Netto, L.E.S.; Nunes, L.R.; Oliveira, R.C.; de Oliveira, M.C.; de Oliveira, R.C.; Pardinho, D.; Pereira, J.C.R.; Rodrigues, V.L.; Rossi, A.; de M. R. Rosa Jr., V.E.; Sala, R.; Setubal, J.C.; Sou
Thomaz, A.M.B.F.; Van Sluys, M.A.; Volpano, M.B.; Wambier, D.S.; Watanabe, M.A.E.; Watanabe, M.H.; Yanai, G.M.; Yarrington, R.; Yoshida, R.H.; Young, M.J.; Zaros, M.C.; Zerlotini, A.; Zingali, R.B.; Van Sluys, M.A.
submitted to GenBank, June 2000
A;Authors: Simpson, A.J.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Arruda, P.; Bonaldo, M.F.; Bonetti, A.M.; Bueno, M.R.; Camargo, A.A.; Camargo, L.E.; Carraro, D.M.; Carrer
as Neto, E.; Dockena, C.; Ferro, E.S.; Ferro, J.A.; Ferro, M.I.; Franco, G.R.; Gruber, A.; Hagler, A.N.; Jorge, J.A.; Kitajima, J.P.; Kobargi, R.; Kuramae, E.E.; Lacerda, G.; Leite, R.P.; Lemos, E.G.; Lemos, M.V.; Machado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Monteiro-Vitorello, C.B.; Moon, D.H.; Nagai, M.A.; Nascimento, A.L.T.O.; Netto, L.E.S.; Nunes, L.R.; Oliveira, R.C.; de Oliveira, M.C.; de Oliveira, R.C.; Pardinho, D.; Pereira, J.C.R.; Rodrigues, V.L.; Rossi, A.; de M. R. Rosa Jr., V.E.; Sala, R.; Setubal, J.C.; Sou
Thomaz, A.M.B.F.; Van Sluys, M.A.; Volpano, M.B.; Wambier, D.S.; Watanabe, M.A.E.; Watanabe, M.H.; Yanai, G.M.; Yarrington, R.; Yoshida, R.H.; Young, M.J.; Zaros, M.C.; Zerlotini, A.; Zingali, R.B.; Van Sluys, M.A.
A;Reference number: A95928
A;Contents: annotation
C;Genetics:
A;Gene: XF2410
C;Superfamily: CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase

Query Match 2.1%; Score 7; DB 2; Length 214
Best Local Similarity [illegible]%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 VAIVPA 195

```
                                                                                
Db      44 VAIVVEA 49


RESULT 36
S45067
probable membrane protein YBR056w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR056C
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 16-Apr-2002
C;Accession: S45067
R;Goffeau, A.; Satchwell, B.; Oberhauer, B.; Straatman, L.
submitted to the Protein Sequence Database, Aug-Dec 1994
A;Reference number: S45067
A;Accession: S45067
A;Molecule type: DNA
A;Residues: 1-214 <GOF>
A;Cross-references: EMBL:z35874; NID:g536754; PID:g536755; PID:g1420
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YBR056w
A;Cross-references: SGD:S0000209
A;Map position: 2R
C;Keywords: transmembrane protein
F;6-65/Domain: transmembrane #status predicted <TMM>

  Query Match              2.1%;  Score 7;  DB 2;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      277 AVIIIII 283
            |||||||
Db      91 AVIIIII 97


RESULT 37
A72008
conserved hypothetical protein CT0231 [imported] - Chlamydia trachomatis (strains CW
N;Alternate names: ct433 hypothetical protein
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 28-Apr-1999 #sequence_revision 28-Apr-1999 #text_change 15-Dec-2000
C;Accession: A72008; B81508
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Hyman, R.W.; Olinger
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis
A;Reference number: A72008; MUID:99269606; PMID:10192387
A;Accession: A72008
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-225 <ARN>
A;Cross-references: GB:AE001637; GB:AE001363; NID:g3329134; NID:g3328
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.; Weidman, J.; Khouri
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Reference number: A61500; MUID:20150295; PMID:10684935
A;Accession: B81508
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-225 <REA>
A;Cross-references: GB:AE002161; GB:AE002160; NID:g3128151; NID:g3128
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CPn0623; "ORF4"

  Query Match              2.1%;  Score 7;  DB 2;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      56 LQAIFSS 62
           |||||||
Db     112 LQAIFSS 118


RESULT 38
F86595
hypothetical protein [imported] - Chlamydophila pneumoniae (strain TW-
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: F86595
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.
Nucleic Acids Res. 28, 2811-2814, 2000
A;Title: Comparison of whole genome sequences of Chlamydia pneumoniae TW-
A;Reference number: A86431; MUID:20335545; PMID:10871402
A;Accession: F86595
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-225 <SHI>
A;Cross-references: GB:AB037696; NID:g3726233; PID:BAA96236.1; GSPDB:GN00161
A;Experimental source: strain TW-
C;Genetics:
A;Gene: CPj0722

  Query Match              2.1%;  Score 7;  DB 2;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      56 LQAIFSS 62
           |||||||
Db     112 LQAIFSS 118


RESULT 39
D96925
probable membrane protein, YrzO family [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: D96925
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Makarova, K.S.; Zeng, Q.; Gibson, R.; L
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacteri
A;Reference number: A96925; MUID:21470962; PMID:11466286
A;Accession: D96925
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-251 <NOL>
A;Cross-references: GB:AE001437; NID:g15894942; PID:AAK79511.1; GSPDB:GN00161
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CA_C0209

  Query Match              2.1%;  Score 7;  DB 2;  Length 251;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      277 AVIIIII 283
            | | | |
Db      8 AVIIIII 14


RESULT 40
S74430
hypothetical protein slr0598 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-1999
C;Accession: S74430
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803 II. Sequence determination of the entire genome and assignment of potential protein-coding regions
A;Reference number: S74422; MUID:97081261; PMID:8905231
A;Accession: S74430
```

A;Title: Novel sequence not shown: translation
A;Molecule type: DNA
A;Residues: 1..33 <KAN>
A;Cross-references: EMBL:[illegible]; NID:[illegible]; PIDN:[illegible]
A;Note: the nucleotide sequence was submitted to the EMBL data library; [illegible]

Query Match 2.1%; Score 7; DB 2; Length [illegible]
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 VLLKPV 44
||||||
Db 46 VLLKIV 52

RESULT 41
[illegible]
hypothetical protein At2g42220 [imported] - Arabidopsis [illegible]
N;Alternate names: hypothetical protein [illegible]
C;Species: Arabidopsis thaliana (mouse ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 25-Mar-2[illegible]
C;Accession: [illegible]
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Creasy, M.L.; Bruni, R.; Dysart, S.M.; Kan, submitted to the EMBL Data Library, December 1997
A;Description: Arabidopsis thaliana chromosome II BAC [illegible] sequence.
A;Reference number: Z14212
A;Accession: [illegible]
A;Status: [illegible] 1-[illegible]-1998
A;Molecule type: DNA
A;Residues: 1..[illegible] <KU>
A;Cross-references: EMBL:[illegible]; NID:[illegible]
A;Experimental source: [illegible]
Kaiho, Y.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.-[illegible]; Fujii, C.Y.; M.; Koo, H.; M.[illegible]; Kotani, H.; Tabata, S.; [illegible]; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, [illegible]; Venter, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A44220; MUID:20084207; PMID:[illegible]
A;Accession: G84851
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1..424 <SU>
A;Cross-references: GB:AE002099; NID:g2765511; PIDN:AAB[illegible]; [illegible]
C;Genetics:
A;Gene: At2g42220; [illegible]
A;Map position: 2
A;Introns: 16/2; 88/1; 109/2; 170/1; 214/1

Query Match 2.1%; Score 7; DB 2; Length [illegible]
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPSPIAL 8
||||||
Db 6 SPSPIAL 12

RESULT 42
[illegible]
Conserved hypothetical protein MTH842 - Methanobacterium [illegible] strain [illegible]
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change [illegible]
C;Accession: [illegible]
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, [illegible]; Lim, D.; Peterson, [illegible]; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, [illegible]; Xiang, K.; Oczkowski, [illegible]; Davis-Hoover, [illegible]; Hsiung, F.; Burykin, [illegible]; Huang, C.-[illegible]; Parokhin, [illegible]; Mao, D.; Owen, [illegible]; Burland, V.; Blattner, F.R.; J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium [illegible]
A;Reference number: A60000; MUID:97457513; PMID:[illegible]
A;Accession: [illegible]
A;Status: preliminary; nucleic acid sequence not shown; [illegible]
A;Molecule type: DNA
A;Residues: 1..[illegible] <MSh>
A;Cross-references: [illegible]
A;Experimental source: strain [illegible]
C;Genetics:
A;Gene: MTH842
A;Start codon: 216
C;Superfamily: conserved hypothetical protein MJ0706

Query Match [illegible]; Score 7; DB 2; Length [illegible]
Best Local Similarity [illegible]; Pred. No. 65;
Matches 7; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

Qy 192 SAESDPL 198
||||||
Db 195 SAESDPL 201

RESULT 43
T32889
hypothetical protein C34B2.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-[illegible]
C;Accession: T32889
R;Chaves, L.; Sulston, J.; Hawkins, M.; Wilson, R.
submitted to the EMBL Data Library, January 1998
A;Description: The sequence of C. elegans cosmid C34B2.
A;Reference number: Z22241
A;Accession: T32889
A;Status: preliminary; translated [illegible]
A;Molecule type: DNA
A;Residues: 1..[illegible] <SAA>
A;Cross-references: [illegible]
A;Experimental source: strain Bristol N2; clone C34B2
C;Genetics:
A;Gene: [illegible]
A;Map position: 1
A;Introns: 45/3; 91/2; 259/

Query Match [illegible]; Score 7; DB 2; Length [illegible]
Best Local Similarity [illegible]; Pred. No. 65;
Matches 7; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

Qy 433 PELPPLP 439
||||||
Db 134 PELPPLP 140

RESULT 44
G02640
Fes/phaRh - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C;Accession: G02640
R;van Dijk, M.A., Morton, J.P., Valderrama, R., Bruekers, M., Heijmans, J.A.M.; Sam submitted to the EMBL Data Library, April 1996
A;Reference number: R01568
A;Accession: G02640
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1..239 <VAN>
A;Cross-references: EMBL:[illegible]; NID:g1262280; PIDN:[illegible]

Query Match 2.1%; Score 7; DB 2; Length [illegible]
Best Local Similarity [illegible]; Pred. No. 66;
Matches 7; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

Qy 199 LELVVTG 204
||||||
Db 119 LELVVTG 124

RESULT 45
[illegible]
hypothetical protein F15C[illegible] - Caenorhabditis elegans

```
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision [Wed Feb 16 #text change [Thu Feb
C;Accession: T20B4
R;Hodgs, T.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z19440
A;Accession: T20B4
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-241 <WIL>
A;Cross-references: EMBL:Z49127; PID:g~AA8804~; GSPDB:GN~ ; ~Caenorhabditis
A;Experimental source: clone B18d2
C;Genetics:
A;Gene: CESP:B18D2.3
A;Map position: 2
A;Introns: 22/2; 209/3

  Query Match              2.1%;  Score 7;  DB 2;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 67;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      118 AQPQPAV 124
            |||||||
Db      134 AQPQPAV 140


RESULT 46
D86623
triosephosphate isomerase (imported) - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: D86623
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Hi
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: D86623
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-251 <Shi>
A;Cross-references: GB:AP000408; NID:g9279436; PID:gBAA0~ ; ~GSPDB:GN~ ; ~
A;Experimental source: strain J138
C;Genetics:
A;Gene: tpiS
C;Superfamily: triose phosphate isomerase

  Query Match              2.1%;  Score 7;  DB 2;  Length 251;
  Best Local Similarity   100.0%;  Pred. No. ~~;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      223 FSEATAE 229
            |||||||
Db      209 FSEATAE 203


RESULT 47
A72000
triosephosphate isomerase - Chlamydophila pneumoniae (strain CWL ~)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-May-2000
C;Accession: A72000
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Hyman, R.; Olinger, L.; Gri
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206806; PMID:10192388
A;Accession: A72000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-254 <AKN>
A;Cross-references: GB:AF085697; GB:AE001670; NID:g4377~; ~NCBI~ ~; ~GSPDB:GN~
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: tpiS
C;Superfamily: triose phosphate isomerase

  Query Match              2.1%;  Score 7;  DB 2;  Length 254;
  Best Local Similarity   100.0%;  Pred. No. ~~;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      223 FSEATAE 229
            |||||||
Db      209 FSEATAE 203


RESULT 48
G81538
triosephosphate isomerase (EC~~) (imported) - Chlamydophila pneumoniae (strain AR39)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 16-May-2000
C;Accession: G81538
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey
, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.; Weidman, J.; Kha
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Reference number: A81538; MUID:20158267; PMID:10684935
A;Accession: G81538
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-254 <READ>
A;Cross-references: GB:AE002161; NID:g4376~; ~GSPDB:GN~ ; ~GSPDB:GN~; PID:g~
A;Experimental source: strain AR39; BL-5 Lsn
C;Genetics:
A;Gene: CPn0786
C;Superfamily: triose-phosphate isomerase

  Query Match              2.1%;  Score 7;  DB 2;  Length 254;
  Best Local Similarity   100.0%;  Pred. No. 67;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      223 FSEATAE 229
            |||||||
Db      209 FSEATAE 203


RESULT 49
G82420
lipase related protein V~A0754 [imported] - Vibrio cholerae (strain N16961 serotype
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: G82420
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
dhanson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
I, R.R.; Mokaltanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae
A;Reference number: A82345; MUID:20406844; PMID:10952301
A;Accession: G82420
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <HEI>
A;Cross-references: GB:AE003854; GB:AE003~; NID:g9656~; ~GSPDB:GN
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0754
A;Map position: 2

  Query Match              2.1%;  Score 7;  DB 2;  Length 276;
  Best Local Similarity   100.0%;  Pred. No. ~~;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      135 QIRYGEL 141
            |||||||
Db       46 QIRYGEL 40


RESULT 50
```

GenCore version [illegible]
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 5, 2002, 06:55:42 ; Search time 34 Seconds
(without alignments)
21.420 Million cell updates/sec

Title: US-09-503-387-3
Perfect score: 849
Sequence: 1 MSFSSPIALI YLGLYIAPVA..... ....KSGTLKIYPS VSPSSLYMG

Scoring table: OLOSUM62
Gapop 60.0 , Gapext 60.0

Searched: 112092 seqs, 41476528 residues

Word size: 3

Total number of hits satisfying chosen parameters: 112092

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 25 summaries

Database: Sequence_DB:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	38	2.9	364	1	KZ3I_HUMAN	[illegible] Homo sapien
2	10	2.9	384	1	KZ3L_HUMAN	[illegible] Homo sapien
3	10	2.9	394	1	KZ3S_HUMAN	[illegible] Homo sapien
4	10	2.9	434	1	KZ34_HUMAN	[illegible] Homo sapien
5	10	2.9	441	1	KZL3_HUMAN	[illegible] Homo sapien
6	10	2.9	448	1	KZL1_HUMAN	[illegible] Homo sapien
7	1	2.9	418	1	KZL2_HUMAN	[illegible] Homo sapien
8	10	2.9	487	1	K3S1_HUMAN	[illegible] Homo sapien
9	10	2.9	444	1	K3L1_HUMAN	[illegible] Homo sapien
10	10	2.9	456	1	K3L2_HUMAN	[illegible] Homo sapien
11	9	2.7	3822	1	ZAP3_HUMAN	[illegible] Homo sapien
12	8	2.4	282	1	INEP_PIG	[illegible] Sus scrofa
13	8	2.4	545	1	PIK_FSVGP	[illegible] Feline sarc
14	8	2.4	892	1	RIP1_MOUSE	[illegible] Mus musculu
15	7	2.1	84	1	Y14D_ARCFU	[illegible] Archaeoglob
16	7	2.1	134	1	PK2C_FEA	[illegible] Felis catus
17	7	2.1	156	1	RISB_CLOAB	[illegible] Clostridium
18	7	2.1	159	1	RISB_STRCN	[illegible] Streptomyces
19	7	2.1	164	1	RISB_SYNY3	[illegible] Synechocyst
20	7	2.1	178	1	IBP1_ARATH	[illegible] Arabidopsis
21	7	2.1	190	1	CKE_SHEEC	[illegible] Sida acuta
22	7	2.1	200	1	PBNH_RHIME	[illegible] Rhizobium m
23	7	2.1	213	1	YSL5_YEAST	[illegible] Saccharomyc
24	7	2.1	217	1	MLG_CANOS	[illegible] Candida obt
25	7	2.1	235	1	Y*SL_SYNY*	[illegible] Synechocyst
26	7	2.1	254	1	IF1S_PICGL	[illegible] Picea glauc
27	7	2.1	261	1	INEP_CERTO	[illegible] Cercocebus
28	7	2.1	281	1	INEP_HUMAN	[illegible] Homo sapien
29	7	2.1	282	1	PTAR_HUMAN	[illegible] Homo sapien
30	7	2.1	304	1	KZS5_HUMAN	[illegible] Homo sapien
31	7	2.1	333	1	CATH_MOUSE	[illegible] Mus musculu
32	7	2.1	343	1	CATH_RAT	[illegible] Rattus norv
33	7	2.1	417	1	Y04*_MELJA	[illegible] Melanoplus
34	7	2.1	42	1	CYZA_CBLVR	[illegible] Chlorohydra
35	7	2.1	459	1	CYS1_RAT	[illegible] Rattus norv
36	7	2.1	469	1	VIL2_HPV30	[illegible] human papil
37	7	2.1	470	1	VIL2_HPV59	[illegible] human papil
38	7	2.1	481	1	EXO*_AZOBR	[illegible] Azospirillu
39	7	2.1	496	1	VNP1_IAB67	[illegible] Influenza a
40	7	2.1	498	1	VNP1_IAB02	[illegible] Influenza a
41	7	2.1	498	1	VNP1_IAK11	[illegible] Influenza a
42	7	2.1	498	1	VNP1_IAM63	[illegible] Influenza a
43	7	2.1	498	1	VNP1_IAM65	[illegible] Influenza a
44	7	2.1	498	1	VNP1_IAM66	[illegible] Influenza a
45	7	2.1	498	1	VNP1_IAM6C	[illegible] Influenza a
46	7	2.1	498	1	VNC1_IAS0P	[illegible] Influenza a
47	7	2.1	498	1	VNC1_IAS11	[illegible] Influenza a
48	7	2.1	498	1	VNC1_IAS61	[illegible] Influenza a
49	7	2.1	498	1	VNC1_IAZDA	[illegible] Influenza a
50	7	2.1	542	1	CXK_HUMAN	[illegible] Homo sapien
51	7	2.1	527	1	CXK_MOUSE	[illegible] Mus musculu
52	7	2.1	529	1	AMD2_HUMAN	[illegible] Homo sapien
53	7	2.1	566	1	KCNI_RAT	[illegible] Rattus norv
54	7	2.1	611	1	CDK5_MUSPF	[illegible] Mustela put
55	7	2.1	614	1	CDK5_HUMAN	[illegible] Homo sapien
56	7	2.1	617	1	FGSH_BOVIN	[illegible] Bos taurus
57	7	2.1	617	1	FGSH_RICPR	[illegible] Rickettsia
58	7	2.1	711	1	VIL2_BPAPS	[illegible] Bacteriophi
59	7	2.1	723	2	IEEM_ADECP	[illegible] Canine aden
60	7	2.1	724	1	CCI1_MOUSE	[illegible] Mus musculu
61	7	2.1	726	1	CCI1_HUMAN	[illegible] Homo sapien
62	7	2.1	727	1	CCI1_HORSE	[illegible] Equus caball
63	7	2.1	730	2	JVL2_HPV30	[illegible] human papil
64	7	2.1	730	2	JVL2_MOUSE	[illegible] Mus musculu
65	7	2.1	755	1	S4L1_HUMAN	[illegible] Homo sapien
66	7	2.1	759	1	YCYL_CAEEL	[illegible] Caenorhabdi
67	7	2.1	772	1	YA4_SCHPO	[illegible] Schizosacch
68	7	2.1	773	1	YAS8_SCHPO	[illegible] Schizosacch
69	7	2.1	827	1	CAS_HALVO	[illegible] Halobacteri
70	7	2.1	873	1	YA7D_SCHPO	[illegible] Schizosacch
71	7	2.1	1*30	1	KSP1_YEAST	[illegible] Saccharomyc
72	7	2.1	1,31	1	ISCA_RAT	[illegible] Rattus norv
73	7	2.1	1257	1	KPB1_RABIT	[illegible] Oryctolagus
74	7	2.1	1,41	1	NFHN_HUMAN	[illegible] Homo sapien
75	7	2.1	1251	1	FOS1_MOUSE	[illegible] Mus musculu

ALIGNMENTS

RESULT 1
KZ3I_HUMAN
ID KZ3I_HUMAN STANDARD; PRT; 364 AA.
AC Q14994; Q14471;
DT 1-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2DS, precursor (MHC class I
DE NK cell receptor Eat-A*11).
GN KIR2DS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=96356237; PubMed=8755891;
RA Blasscol K., Cattoni G., Faure M., Vendiani S., Ottolenghi C., Viltalo M.,
RA Coulie P., Poggi A., Moretta L.;
RT "The human leukocyte antigen (HLA)-C-specific "activatory" or
RT "inhibitory" natural killer cell receptors display highly homologous
RT extracellular domains but differ in their transmembrane and
RT intracytoplasmic portions.";
RL J. Exp. Med. 184:475-483(1996).
RN [2]

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SQ   SEQUENCE FROM N.A.; AND VARIANTS.
RX   MEDLINE 96010086; PubMed 8521221;
RA   Uhrberg M., Valiante N.M., Shum B.P., Parham P.;
RA   Lienert Wendenbach K., Cortiss R., Lyon D., Lander L.L., Lanier L.L.;
RT   "Human diversity in killer cell inhibitory receptor genes.";
RL   Immunity 7:753-763(1997).
CC   -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-A ALLELES.
CC       DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2 TYPE 1 DOMAINS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X96926; CAA65482.1; -.
DR   EMBL; AF022365; AAB95019.1; -.
DR   HSSP; P43629; 1NKR.
DR   Genew; HGNC:7933; KIR2DS1.
DR   MIM; 604953; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW   Repeat; Multigene family; Polymorphism.
FT   SIGNAL       1     21       BY SIMILARITY.
FT   CHAIN       22    304       KILLER-CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT                               2DS2.
FT   DOMAIN      22    245       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   246    266       POTENTIAL.
FT   DOMAIN     267    304       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      42    107       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN     142    205       IG-LIKE C2-TYPE DOMAIN 2.
FT   DISULFID    49    100       BY SIMILARITY.
FT   DISULFID   149    198       BY SIMILARITY.
FT   CARBOHYD    64     64       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   176    176       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   211    211       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARIANT     91     91       R -> K.
FT                               /FTId=VAR_010516.
SQ   SEQUENCE   304 AA;  33946 MW;  4194A9421E15AE96 CRC64;

  Query Match             2.9%;  Score 10;  DB 1;  Length 304;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     115 KESLSAQEGE 124
           ||||||||||
Db     108 KESLSAQEGE 117


RESULT 2
K2S2_HUMAN
ID   K2S2_HUMAN     STANDARD;      PRT;   304 AA.
AC   P43629, Q14955;
DT   01-NOV-1995 (Rel. 32, Created)
DT   26-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2003 (Rel. 41, Last annotation update)
DE   Killer-cell immunoglobulin-like receptor 2DS2 precursor (CD158 ...
DE   NK cell receptor) (Natural killer-associated transcript 5) (NKAT5).
DE   Zp58 natural killer cell receptor clone CL-49) (p58 NK receptor) (NK
DE   receptor loc A-1).
GN   KIR2DS2 OR NKAT5.
OS   Homo sapiens (Human).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 2-304 FROM N.A.
RC   TISSUE=Natural killer cells;
RX   MEDLINE=96010086; PubMed=8521221;
RA   Uhrberg M., Valiante N.M., Shum B.P., Parham P.;
RA   Lienert-Wendenbach K., Cortiss R., Lyon D., Lander L.L., Lanier L.L.;
RT   "Human diversity in killer cell inhibitory receptor genes.";
RL   Immunity 7:753-763(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95252524; PubMed=7716543;
RA   Colonna M., Samaridis J.;
RT   "Cloning of immunoglobulin-superfamily members associated with HLA-C
RT   and HLA-B recognition by human natural killer cells.";
RL   Science 268:405-408(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoid;
RX   MEDLINE=96196217; PubMed=8621776;
RA   Biassoni R., Cantoni C., Falco M., Verdiani S., Bottino C., Vitale M.,
RA   Conte R., Pende A., Moretta A., Moretta L.;
RT   "The human leukocyte antigen (HLA)-C specific 'receptors' in
RT   'inhibitory' natural killer cells recognize polymorphic framework
RT   extracellular domains but differ in their transmembrane and
RT   intracytoplasmic portions.";
RL   J. Exp. Med. 183:645-650(1996).
CC   -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-A ALLELES.
CC       DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2 TYPE 1 DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U24079; AAC50386.1; ALT_INIT.
DR   EMBL; Z75330; CAA99225.1; -.
DR   EMBL; X96926; CAA65482.1; -.
DR   HSSP; P43629; 1NKR.
DR   Genew; HGNC:7933; KIR2DS2.
DR   MIM; 604953; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
KW   Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW   Repeat; Multigene family.
FT   SIGNAL       1     21       BY SIMILARITY.
FT   CHAIN       22    304       KILLER-CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT                               2DS2.
FT   DOMAIN      22    245       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   246    266       POTENTIAL.
FT   DOMAIN     267    304       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      42    107       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN     142    205       IG-LIKE C2-TYPE DOMAIN 2.
FT   DISULFID    49    100       BY SIMILARITY.
FT   DISULFID   149    198       BY SIMILARITY.
FT   CARBOHYD    64     64       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   176    176       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   211    211       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT    20     21       WA -> G (IN REF. 3).
SQ   SEQUENCE   304 AA;  33946 MW;  4194A9421E15AE96 CRC64;
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  Query Match             2.0%;  Score 7.;  DB 1;  Length 5.
  Best Local Similarity   100.0%;  Pred. No. 2.6e-;
  Matches   [0];  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      113 KPSESAQPGP 122
            ||||||||||
Db      128 KPSESAQPGP 137


RESULT 3
KJ5A_HUMAN
ID   KJ5A_HUMAN      STANDARD;      PRT:   344 AA.
AC   Q14952;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Killer cell immunoglobulin-like receptor 2DS4 precursor (MHC class I
DE   NK cell receptor) (Natural killer associated transcript 5) (NKAT-5).
GN   KIR2DS4 OR NKAT5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoid;
RA   Blasson M.;
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS THAT BIND HLA-A ALLELES.
CC       DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2 TYPE DOMAINS.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announ
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U76832; AAB-----.1; -.
DR   EMBL; X92221; CAA63227.1; -.
DR   PIR; S48626; S48626.
DR   MGD; MGI:1338876; Kir2ds4.
DR   MIM; 604934; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IGc2_like; 1.
KW   Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW   Type-2 membrane family.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    344       KILLER CELL IMMUNOGLOBULIN-LIKE
FT                                2DS4.
FT   DOMAIN       22    115       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    116    136       POTENTIAL.
FT   DOMAIN      137    344       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42    107       IG-LIKE C2-TYPE 1 MAIN.
FT   DOMAIN      112    205       IG-LIKE C2-TYPE 2 MAIN.
FT   DISULFID     49    100       BY SIMILARITY.
FT   DISULFID    118    193       BY SIMILARITY.
FT   CARBOHYD     84     84       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   344 AA;  37826 MW;  B0F93E7D9441E87E CRC64;

  Query Match             2.0%;  Score 7.;  DB 1;  Length 5.4;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-;
  Matches   [0];  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      113 KPSESAQPGP 122
            ||||||||||
Db      128 KPSESAQPGP 137


RESULT 4
KJ2S_HUMAN
ID   KJ2S_HUMAN      STANDARD;      PRT:   344 AA.
AC   Q14954;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Killer cell immunoglobulin-like receptor 2DS4 precursor (MHC class I
DE   NK cell receptor) (Natural killer associated transcript 5) (NKAT-5)
DE   (p58 natural killer cell receptor clone CL-5) (p58 NK receptor) (CL
DE   1).
GN   KIR2DS4 OR NKAT5 OR KKA5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Natural killer cells;
RX   MEDLINE=96269128; PubMed=8749883;
RA   Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Malnati M.S.,
RA   Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT   "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RT   related molecules with diversity in both the extra- and intracellular
RT   domains.";
RL   Immunity 2:439-449(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoid;
RX   MEDLINE=96270004; PubMed=8765626;
RA   Bottino C., Sivori S., Vitale M., Cantoni C., Falco M., Pende D.,
RA   Morelli L., Augugliaro R., Semenzato G., Biassoni R., Moretta L.,
RA   Moretta A.;
RT   "A novel surface molecule homologous to the p70/p58 family of
RT   receptors is selectively expressed on a subset of human natural
RT   killer cells and induces both triggering of cell functions and
RT   proliferation.";
RL   Eur. J. Immunol. 25:2655-2661(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Chan H.W., Colter K.L.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS THAT BIND HLA-A ALLELES.
CC       DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IGM N-GLYCOLIN LIKE C2 TYPE D MAINS.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
```

```
CC
DR   EMBL; S24017; AAC99496.1; ALT_INIT.
DR   EMBL; L76571; AAB60600.1; -.
DR   EMBL; X90851; CAA62472.1; -.
DR   EMBL; AF022950; AAB61280.1; -.
DR   HSSP; P43626; 1NKR.
DR   Genew; HGNC:6338; KIR2DS4.
DR   MIM; 604945; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
KW   Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW   Repeat; Multigene family.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    304       KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT                                 2DS4.
FT   DOMAIN       22    215       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    216    265       POTENTIAL.
FT   DOMAIN      266    304       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42    107       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN      142    205       IG-LIKE C2-TYPE DOMAIN 2.
FT   DISULFID     49    107       BY SIMILARITY.
FT   DISULFID    149    198       BY SIMILARITY.
FT   CARBOHYD     97     97       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     84     84       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    114    114       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    178    178       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    211    211       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   304 AA;  33760 MW;  7FFDAFE5DC7DAAF4 CRC64;

  Query Match             2.9%;  Score 10;  DB 1;  Length 304;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      115 KPSLSAQPGP 124
            ||||||||||
Db      198 KPSLSAQPGP 207


RESULT 5
KIR3_HUMAN
ID   KIR3_HUMAN     STANDARD;      PRT:   447 AA.
AC   P43626; Q14847;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JAN-2002 (Rel. 41, Last annotation update)
DE   Killer cell immunoglobulin-like receptor 2DL3 precursor (MHC class I
DE   NK cell receptor) (Natural killer associated transcript 2) (NKAT2)
DE   (p58 natural killer cell receptor clone CL-6) (p58 NK receptor) (p58
DE   MHC class I-specific NK receptor).
GN   KIR2DL3 OR NKAT2 OR P58NKR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Natural killer cells;
RX   MEDLINE=95242525; PubMed=7716544;
RA   Colonna M., Samaridis J.;
RT   "Cloning of immunoglobulin-superfamily members associated with HLA
RT   and MHC class I are recognized by human natural killer cells.";
RL   Science 268:405-408(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Natural killer cells;
RX   MEDLINE=97269128; PubMed=9149900;
RA   Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Malnati M.S.,
RA   Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT   "Molecular clones of the p58 NK cell receptor reveal immunoglobulin
RT   related molecules with diversity in both the extra- and intracellular
RT   domains.";
RL   Immunity 2:439-449(1995).
RN   [3]
RP   SEQUENCE FROM N.A., AND VARIANT.
RX   MEDLINE=98050965; PubMed=9435221;
RA   Uhrberg M., Valiante N.M., Shum B.P., Shilling H.G.,
RA   Lienert-Weidenbach K., Corliss B., Tyan D., Lanier L.L., Parham P.;
RT   "Human diversity in killer cell inhibitory receptor genes.";
RL   Immunity 7:753-763(1997).
CC   -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC       INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC    !  SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC    !  SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L41268; AAA98805.1; -.
DR   EMBL; S24024; AAB05321.1; -.
DR   EMBL; AF022948; AAB95321.1; -.
DR   HSSP; P43626; 1NKR.
DR   Genew; HGNC:6343; KIR2DL3.
DR   MIM; 604937; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
KW   Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW   Repeat; Multigene family; Polymorphism.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    341       KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT                                 2DL3.
FT   DOMAIN       22    119       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    120    140       POTENTIAL.
FT   DOMAIN      141    341       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42    102       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN      142    205       IG-LIKE C2-TYPE DOMAIN 2.
FT   DISULFID     49    107       BY SIMILARITY.
FT   DISULFID    149    198       BY SIMILARITY.
FT   CARBOHYD     84     84       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    178    178       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    211    211       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARIANT       9      9       V -> A.
FT                                 /FTId=VAR_01045.
FT   VARIANT      32     32       I -> F.
FT                                 /FTId=VAR_012754.
FT   VARIANT      54     54       Q -> E.
FT                                 /FTId=VAR_012755.
FT   VARIANT      71     71       R -> K.
FT                                 /FTId=VAR_01046.
FT   VARIANT     153    153       F -> S.
FT                                 /FTId=VAR_012756.
SQ   SEQUENCE   341 AA;  37866 MW;  C1DA8F1 CRC64;

  Query Match             2.9%;  Score 10;  DB 1;  Length 341;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      115 KPSLSAQPGP 124
            ||||||||||
Db      128 KPSLSAQPGP 137


RESULT 6
KIL1_HUMAN
ID   KIL1_HUMAN     STANDARD;      PRT:   444 AA.
AC   P43628;
DT   01-NOV-1995 (Rel. 32, Created)
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ID   01 NOV 1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Killer cell immunoglobulin-like receptor 2DL2 precursor (CD158 cl
DE   NK cell receptor) (Natural killer associated transcript 2) (NKAT-2
DE   (p58 natural killer cell receptor clone CL-42/1.1) (p58 NK
DE   receptor) (p58.1 MHC class I specific NK receptor).
GN   KIR2DL2 OR NKAT2 OR CD158A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Natural killer cells;
RX   MEDLINE=95269128; PubMed=7719980;
RA   Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Malnati M.S.,
RA   Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT   "Molecular clones of the p58 NK cell receptor reveal immunoglobulin
RT   related molecules with diversity in both the extra- and intracellular
RT   domains.";
RL   Immunity 2:439-449(1995).
RN   [2]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 22-47.
RC   TISSUE=Natural killer cells;
RX   MEDLINE=94243449; PubMed=7911994;
RA   Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Malnati M.S.,
RA   Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT   "Molecular clones of the p58 NK cell receptor reveal immunoglobulin
RT   related molecules with diversity in both the extra- and intracellular
RT   domains.";
RL   Immunity 2:439-449(1995).
RN   [3]
RP   SEQUENCE FROM N.A., AND VARIANTS.
RX   MEDLINE=96176096; PubMed=8643422;
RA   Uhrberg M., Valiante N.M., Shum B.P., Shilling H.G.,
RA   Lienert-Weidenbach K., Corliss B., Tyan D., Lanier L.L., Parham P.;
RT   "Human diversity in killer cell inhibitory receptor genes.";
RL   Immunity 7:753-763(1997).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cytotoxic T-cell clone;
RX   MEDLINE=94143445; PubMed=8299975;
RA   Pende D., Marcenaro S., Falco M., Martini S., Bernardo M.E.,
RA   Montagna D., Romeo E., Cognet C., Martinetti M., Maccario R.,
RA   Mingari M.C., Vivier E., Moretta L., Moretta A., Moretta L.;
RT   "Anti-HLA class I inhibitory receptors. Individual
RT   specificities recognize molecules of HLA-B and HLA-C serologically
RT   defined subsets. Comparison with specificities mediating
RT   alloreactivity in human CD3- CD16+ natural killer cells.";
RL   J. Exp. Med. 179:1023-1028(1994).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Natural killer cell;
RX   MEDLINE=94343335; PubMed=8089975;
RA   Fan Z.G., Moysyuk L., Winter C.C., Wagtmann N., Long E.O.,
RA   Parham P.;
RT   "Structure of the inhibitory receptor for human natural killer cells
RT   resembles haematopoietic receptors.";
RL   Nature 370:496-498(1994).
CC   -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS WHICH
CC       INHIBITS THE ACTIVITY OF NK CELLS UPON ENGAGEMENT WITH
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE 1 DOMAINS.
CC   ---------- ----------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------- ----------
DR   EMBL; L41267; AAA60878.1; -.
DR   EMBL; U24076; AAC50366.1; -.
DR   EMBL; U24078; AAC50367.1; -.
DR   EMBL; AF022945; AAB95-19.1; -.
DR   PDB; 1NKR; 11-NOV-98.
DR   GenCore_DBNO; GC_DBNO_2.
DR   MIM; 604946; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW   Repeat; Multigene family; Polymorphism; Secreted.
FT   SIGNAL       1     21
FT   CHAIN        22    318       KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT                                 2DL2.
FT   DOMAIN       22    119       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     246   268       POTENTIAL.
FT   DOMAIN       269   318       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42    107       IG LIKE C2 TYPE 1 DOMAIN 1.
FT   DOMAIN       142   205       IG LIKE C2-TYPE DOMAIN 2.
FT   DISULFID     49    103
FT   DISULFID     149   198
FT   CARBOHYD     67    67        N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     84    84        N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     144   144       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     178   178       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARIANT       5     5         S -> F.
FT                                 /FTId=VAR_000949.
FT   VARIANT      47    47        R -> K.
FT                                 /FTId=VAR_000950.
FT   VARIANT      145   145       I -> L.
FT                                 /FTId=VAR_000951.
FT   VARIANT      175   175       I -> T.
FT                                 /FTId=VAR_
FT   VARIANT      184   184       S -> N.
FT                                 /FTId=VAR_
FT   VARIANT      223   223       R -> K.
FT                                 /FTId=VAR_000952.
FT   VARIANT      237   237       K -> E.
FT                                 /FTId=VAR_000953.
FT   VARIANT      256   256       E -> G.
FT                                 /FTId=VAR_000954.
SQ   SEQUENCE   448 AA;  50506 MW;  4BBBE2DCEDFEF8DE CRC64;

  Query Match              [illegible]%;  Score [illegible];  DB 1:  [illegible] 448;
  Best Local Similarity    [illegible]%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy      [illegible] KPSLSAQLGP 122
                ||||||||||
Db      [illegible] KPSLSAQLGP 147


RESULT 2
KZL2_HUMAN
ID   KZL2_HUMAN      [illegible]      [illegible]      [illegible] AA.
AC   Q63627; Q14951;
DT   01-NOV-1996 (Rel. 32, Created)
DT   01-NOV-1996 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Killer cell immunoglobulin-like receptor 2DL2 precursor (CD158 cl
DE   NK cell receptor) (Natural killer associated transcript 2) (NKAT-2
DE   (p58 natural killer cell receptor clone CL-42/1.1) (p58 NK receptor).
GN   KIR2DL2 OR NKAT2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Natural killer cells;
RX   MEDLINE=95269128; PubMed=7719980;
RA   Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Malnati M.S.,
RA   Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT   "Molecular clones of the p58 NK cell receptor reveal immunoglobulin
RT   related molecules with diversity in both the extra- and intracellular
RT   domains.";
RL   Immunity 2:439-449(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96176096; PubMed=8643422;
RA   Uhrberg M., Valiante N.M., Shum B.P., Shilling H.G.,
RA   Lienert-Weidenbach K., Corliss B., Tyan D., Lanier L.L., Parham P.;
RT   "Human diversity in killer cell inhibitory receptor genes.";
RL   Immunity 7:753-763(1997).
CC   -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS WHICH
CC       INHIBITS THE ACTIVITY OF NK CELLS UPON ENGAGEMENT WITH
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```
XX       CELLULAR.
XX     !  SUBCELLULAR LOCATION: Type I membrane protein.
XX     !  SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
XX     !  SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN LIKE C2 TYPE DOMAINS.
XX
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XX   or send an email to license@isb-sib.ch).
XX
DR   EMBL; U21049; AAB05334.1; -.
DR   EMBL; L76669; AAC00672.1; -.
DR   HSSP; P43626; 1NKR.
DR   GeneW; HGNC:9340; KIR3DL2.
DR   MIM; 604937; -.
DR   InterPro; IPR003006; Ig.
DR   InterPro; IPR003599; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
KW   Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW   Repeat; Multigene family.
FT   SIGNAL          1     21       BY SIMILARITY.
FT   CHAIN          22    418       KILLER-CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT                                  2DL2.
FT   DOMAIN         22    115       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      239    261       POTENTIAL.
FT   DOMAIN        262    418       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN         32    107       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN        132    206       IG-LIKE C2-TYPE DOMAIN 2.
FT   DISULFID       47    100       BY SIMILARITY.
FT   DISULFID      149    198       BY SIMILARITY.
FT   CARBOHYD       84     84       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      178    178       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      271    271       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT      269    269       SER -> PRO (IN REF. 2).
SQ   SEQUENCE   418 AA;  47172 MW;  7B43F5A0F5C72F6A CRC64;

  Query Match             2.9%;  Score 10;  DB 2;  Length 418;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      113 KPSLSAEPGP 122
            ||||||||||
Db      206 KPSLSAEPGP 215


RESULT 8
K4SL_HUMAN
ID   K4SL_HUMAN      STANDARD;      PRT;   367 AA.
AC   Q13956;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Killer cell immunoglobulin-like receptor 3DL2 precursor (MHC class I
DE   NK cell receptor) (Natural killer-associated transcript 5) (NKAT-5).
GN   KIR3DL2 OR NKAT5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98239034; PubMed=9682009;
RA   Uhrberg M., Valiante N.M., Shum B.P., Shilling H.G.,
RA   Lienert-Weidenbach K., Corliss B., Tyan D., Lanier L.L., Parham P.;
RT   "Human diversity in killer cell inhibitory receptor genes.";
RL   Immunity 7:753-763(1997).
CC   -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-A*11 ALLELES.
CC       DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN LIKE C2 TYPE DOMAINS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L76669; AAB06584.1; -.
DR   HSSP; P43626; 1NKR.
DR   GeneW; HGNC:9340; KIR3DL2.
DR   MIM; 604937; -.
DR   InterPro; IPR003006; Ig.
DR   InterPro; IPR003599; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
KW   Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW   Repeat; Multigene family; Polymorphism.
FT   SIGNAL          1     21       BY SIMILARITY.
FT   CHAIN          22    387       KILLER-CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT                                  3DL2.
FT   DOMAIN         22    115       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      211    233       POTENTIAL.
FT   DOMAIN        234    387       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN         42    102       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN        137    202       IG-LIKE C2-TYPE DOMAIN 2.
FT   DOMAIN        237    300       IG-LIKE C2-TYPE DOMAIN 3.
FT   DISULFID       47     95       BY SIMILARITY.
FT   DISULFID      144    195       BY SIMILARITY.
FT   DISULFID      244    295       BY SIMILARITY.
FT   CARBOHYD       92     92       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      179    179       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      271    271       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARIANT       166    166       R -> H.
FT                                  /FTId=VAR_010477.
SQ   SEQUENCE   387 AA;  42502 MW;  9E75B7843B1F6100 CRC64;

  Query Match             2.9%;  Score 10;  DB 8;  Length 387;
  Best Local Similarity   100.0%;  Pred. No. 0.32;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      113 KPSLSAEPGP 122
            ||||||||||
Db      223 KPSLSAEPGP 232


RESULT 9
K4SI_HUMAN
ID   K4SI_HUMAN      STANDARD;      PRT;   444 AA.
AC   P43626; Q16541; O43427;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Killer cell immunoglobulin-like receptor 3DL1 precursor (MHC class I
DE   NK cell receptor) (Natural killer-associated transcript 5) (NKAT-5)
DE   (p70 natural killer cell receptor clone CL-2/3.1) (BELA BW1 specific
DE   inhibitory NK cell receptor).
GN   KIR3DL1 OR NKAT5 OR NKB1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RT   "Cloning of immunoglobulin superfamily members associated with HLA-
RT   and HLA B recognition by human natural killer cells.";
RL   Science 256:405-408(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood lymphocytes;
RX   MEDLINE=92327526; PubMed=1378643;
RA   Wagtmann N., Rajagopalan S., Winter C.C., Peruzzi M., Long E.O.;
RT   "Killer cell inhibitory receptors specific for HLA-C and HLA-B
RT   identified by direct binding and by functional transfer.";
RL   Immunity 3:801-809(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood lymphocyte;
RX   MEDLINE=97078052; PubMed=7526744;
RA   D'Andrea A., Chang C., Franz Bacon K., McClanahan T., Phillips J.H.,
RA   Lanier L.L.;
RT   "Molecular cloning of NKB1. A natural killer cell receptor for HLA-B
RT   allotypes.";
RL   J. Immunol. 155:2306-2310(1995).
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANTS.
RX   MEDLINE=96079086; PubMed=9433221;
RA   Uhrberg M., Valiante N.M., Shum B.P., Shilling H.G.,
RA   Lienert-Weidenbach K., Corliss B., Tyan D., Lanier L.L., Parham P.;
RT   "Human diversity in killer cell inhibitory receptor genes.";
RL   Immunity 7:753-763(1997).
CC   -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS. ITS
CC       ACTIVE, INHIBITS THE ACTIVITY OF NK CELLS (ITS INVOLVED
CC       CELL LYSIS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE (I-SET) DOMAINS.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J11263; AAA59870.1.  -.
DR   EMBL; U90273; AAB52521.1.  -.
DR   EMBL; U56274; AAB52522.1.  -.
DR   EMBL; X91203; CAA62938.1.  -.
DR   EMBL; U83146; AAC24725.1.  -.
DR   EMBL; AF022949; AAB95322.1.  -.
DR   HSSP; P43629; 1NKR.
DR   GDB; 9507933; KIR3DL1.
DR   MIM; 604946; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
KW   Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW   Repeat; Multigene family; Polymorphism.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    444       KILLER-CELL IMMUNOGLOBULIN-LIKE
FT                                RECEPTOR 3DL1 PRECURSOR.
FT   DOMAIN       22    84        EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     85    107       POTENTIAL.
FT   CYTOPLASMIC  108   444       POTENTIAL.
FT   DOMAIN       22    122       IG-LIKE C2-TYPE 1 (MAIN) 1.
FT   DOMAIN       127   202       IG-LIKE C2-TYPE 2 (MAIN) 2.
FT   DOMAIN       237   306       IG-LIKE C2-TYPE 3 (MAIN) 3.
FT   DISULFID     49    107       BY SIMILARITY.
FT   DISULFID     144   187       BY SIMILARITY.
FT   DISULFID     244   293       BY SIMILARITY.
FT   CARBOHYD     92    92        N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     179   179       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     278   278       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARIANT      2     2         S -> N.
FT                                /FTId=VAR_003812.
FT   VARIANT      13    13        S -> P.
FT                                /FTId=VAR_003813.
FT   VARIANT      23    23        M -> V.
FT                                /FTId=VAR_003814.
FT   VARIANT      88    88        I -> V.
FT                                /FTId=VAR_003815.
FT   VARIANT      99    99        L -> I.
FT                                /FTId=VAR_003816.
FT   VARIANT      299   299       I -> R.
FT                                /FTId=VAR_003817.
FT   VARIANT      333   333       S -> C.
FT                                /FTId=VAR_003818.
SQ   SEQUENCE   444 AA;  [illegible]
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Query Match 2.4%; Score 10; DB 2; Length 444;
Best Local Similarity 3.1%; Pred. No. 0.042;
Matches 10; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy     113 KESESAQPGP 122
           ||||||||||
Db     222 KESESAQPGP 231
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RESULT 10
KK2_HUMAN
ID   KK2_HUMAN STANDARD; PRT; 447 AA.
AC   P43631; Q13238; Q92604; Q14943; Q14948;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Killer cell immunoglobulin-like receptor 2DL2 precursor (MHC class I
DE   NK cell receptor) (Natural killer associated transcript 4) (NKAT4)
DE   (p70 natural killer cell receptor clone 7.6).
GN   KIR2DL2 OR NKAT4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Natural killer cells;
RX   MEDLINE=95342526; PubMed=7543943;
RA   Colonna M., Samaridis J.;
RT   "Cloning of immunoglobulin-superfamily members associated with HLA-C
RT   and HLA-B recognition by human natural killer cells.";
RL   Science 268:405-408(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood lymphocytes;
RX   MEDLINE=96111997; PubMed=8777725;
RA   Wagtmann N., Rajagopalan S., Winter C.C., Peruzzi M., Long E.O.;
RT   "Killer cell inhibitory receptors specific for HLA-C and HLA-B
RT   identified by direct binding and by functional transfer.";
RL   Immunity 3:801-809(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoid;
RX   MEDLINE=96345801; PubMed=8764004;
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RA   Pende D., Biassoni R., Cantoni C., Verdiani S., Falco M.,
RA   di Donato C., Accame L., Bottino C., Moretta A., Moretta L.;
RT   "The natural killer cell receptor specific for HLA-A allotypes:
RT   a novel member of the p58/p70 family of inhibitory receptors
RT   characterized by three immunoglobulin-like domains and is expressed as
RT   a 140-kD disulphide-linked dimer.";
RL   J. Exp. Med. 184:505-518(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96276008; PubMed=8643091;
RA   Gobbini C., Samaridis J., Colonna M.;
RT   "Alternatively spliced forms of human killer inhibitory receptor.";
RL   Immunogenetics 44:227-230(1996).
RN   [5]
RP   VARIANTS.
RX   MEDLINE=96060005; PubMed=8540221;
RA   Barbera M., Villanueva N.M., Shum B.P., Skilling H.,
RA   Lienert Weidenbach K., Corliss B., Ivan D., Lanier L.L., Parham P.;
RT   "Human diversity in killer cell inhibitory receptor genes.";
RL   Immunity 3:755-769(1995).
CC   -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS. B-A-A ALLELES.
CC       INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2 TYPE DOMAINS.
CC   ---------- ----- ---------- -----
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CC   or send an email to license@isb-sib.ch).
CC   ---------- ----- ----------
DR   EMBL; X81776; CAA57011.1; -.
DR   EMBL; D30775; BAA05206.1; -.
DR   EMBL; X76534; CAA54011.1; -.
DR   EMBL; L76669; AAB39594.1; -.
DR   EMBL; U76832; AAB35401.1; -.
DR   HSSP; P43626; 1NKB.
DR   Genew; HGNC:7679; KIR2DL2.
DR   MIM; 604937; -.
DR   InterPro; IPR003006; Ig.
DR   InterPro; IPR003599; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 3.
KW   Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW   Repeat; Multigene family; Polymorphism.
FT   SIGNAL       1     21       BY SIMILARITY.
FT   CHAIN       22    499       KILLER-CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT                               2DL2.
FT   DOMAIN       22    94       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    111   133       POTENTIAL.
FT   DOMAIN      134   499       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42   102       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN      142   202       IG-LIKE C2-TYPE DOMAIN 2.
FT   DOMAIN      237   305       IG-LIKE C2-TYPE DOMAIN 3.
FT   DISULFID     49    95       BY SIMILARITY.
FT   DISULFID    144   196       BY SIMILARITY.
FT   DISULFID    244   293       BY SIMILARITY.
FT   CARBOHYD    179   179       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    249   249       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    275   275       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    305   305       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARIANT      43    43       P -> A.
FT                               /FTId=VAR_010625.
FT   VARIANT     113   113       I -> V.
FT                               /FTId=VAR_010626.
FT   VARIANT     158   158       E -> G.
FT                               /FTId=VAR_010627.
FT   VARIANT     166   166       K -> N.
FT                               /FTId=VAR_010628.
FT   VARIANT     228   228       A -> P.
FT                               /FTId=VAR_010629.
FT   VARIANT     252   252       I -> T.
FT                               /FTId=VAR_010630.
SQ   SEQUENCE   499 AA;  [illegible] MW;  [illegible] CRC64;

  Query Match             [illegible]; Score [illegible]; DB 6; Length 499;
  Best Local Similarity   [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy      [illegible] KESLSAQPSP [illegible]
        [illegible]
Db      223 KESLSAQPSP 232


RESULT 11
ZAP7_HUMAN
ID   ZAP7_HUMAN      STANDARD;      PRT:  1822 AA.
AC   P49750; P49752; Q96IV7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Nuclear protein ZAP7 (ZAP70).
GN   ZAP7.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   [illegible], Mitsu A., [illegible], Mikal M., Sarabia..., Li, Bradtke B.,
RA   Bloom S., Ivars M., Dickhoff R., Fleetwood P., Harrison G., Times P.,
RA   Kaur S., Madu S., ..., M.P., Saterlie A., Statter I., Bood L.;
RT   "Sequencing of human chromosome 14q24.3 region.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 539-847 AND 1697-1822 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=95310522; PubMed=7596407;
RA   Sherrington R., Rogaev E.I., Liang Y., Rogaeva E.A., Levesque G.,
RA   Ikeda M., Chi H., Lin C., Li G., Holman K., Tsuda T., Mar L.,
RA   Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rainero I.,
RA   Pinessi L., Nee L., Chumakov I., Pollen D., Brookes A.,
RA   Sanseau P., Polinsky R.J., Wasco W., Da Silva H.A.R., Haines J.L.,
RA   Perkicak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E.,
RA   Rommens J.M., St George-Hyslop P.H.;
RT   "Cloning of a gene bearing missense mutations in early-onset familial
RT   Alzheimer's disease.";
RL   Nature 375:754-760(1995).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- CAUTION: Bot.2 sequence differs from that shown due to a
CC       frameshift in position 1656).
CC   ---------- --
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CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; AC012076; AAF61275.1; -.
DR   EMBL; AF4364; AAM12881.1; ALT_FRAME.
DR   EMBL; Z48482; AAC42046.1; -.
KW   Nuclear protein.
FT   DOMAIN       15    207       IRS-BIND.
FT   DOMAIN      382    430       SLN-BIND.
FT   DOMAIN      807   1209       ABP-BIND.
FT   DOMAIN     1466   1577       ABP-BIND.
FT   CONFLICT    621    623       P -> S (IN REF. 2).
FT   CONFLICT   1454   1484       I -> T (IN REF. 2).
FT   CONFLICT   1821   1821       K -> E (IN REF. 2).
SQ   SEQUENCE  1822 AA;  [illegible] MW;  [illegible] CRC64;
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  Query Match             2.7%;  Score 76;  DB 1;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   76;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      208 KIPPEPILE 216
            |||||||||
Db      134 KIPPEPILE 126


RESULT 2
INFB_HUMAN
ID   INFB_HUMAN      STANDARD;      PRT:   242 AA.
AC   P28562; Q96CN1; Q96MB4;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 6 precursor
DE   (Ligand).
GN   INFSF6 OR FASL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; ...
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21122655; PubMed=11423111;
RA   Mimata Y., Shimoji Y., Inomata S., Mori Y.,
RT   "Molecular cloning, characterization, and expression of the rat Fas
RT   ligand (CD95 ligand).";
RL   J. Interferon Cytokine Res. 21:805-812(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Small Asian miniature pig;
RA   Zhu N., Yoshie Y.;
RT   "Molecular cloning and characterization of porcine Fas ligand cDNA.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoma;
RA   Isoyoki S., Kono M., Bloom E.T.;
RT   "Cloning and potential utility of porcine Fas ligand: ...";
RT   In porcine ocular protects them from attack by human ...";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Caribou x Large Yorkshire white; TISSUE=Liver;
RX   PubMed=11792626;
RA   Mohori-Ishiyama Y., Nakajima Y., Koba S., Iwasaki Y.,
RT   "Porcine Fas-ligand gene: genomic sequence analysis and ...";
RT   with human gene.";
RL   Mol. Immunol. 39:581-589(2002).
CC   -!- FUNCTION: Cytokine that binds to INFRSF6/FAS, a receptor ...
CC       transduces the apoptotic signal into cells. May be ...
CC       cytotoxic T cell mediated apoptosis and in T cell ...
CC       INFSF6/FAS mediated apoptosis may have a role in the control ...
CC       peripheral tolerance, in the antigen stimulated ... T ...
CC       T cells, or both. Binding to the decoy receptor ... INFRSF6/FAS
CC       modulates its effects (by similarity).
CC   -!- SUBUNIT: Homotrimer (Probable).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (by ...
CC       similarity).
CC   -!- INDUCTION: By IL-2.
CC   -!- PTM: The soluble form derives from the membrane ...
CC       proteolytic processing (by similarity).
CC   -!- SIMILARITY: BELONGS TO THE TNF FAMILY. ...
CC   ---------- ---------- ---------- ----------
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CC                                                  ---         ---         ----
DR   EMBL; AB027297; BAB40916.1;
DR   EMBL; AY101644; AAK56446.1;
DR   EMBL; AF327402; AAK84435.1;
DR   EMBL; AB069764; BAB64249.1; -.
DR   HSSP; P01375; 4ISV.
DR   InterPro; IPR006396; INF_fam.
DR   InterPro; IPR008983; INF_family
DR   Pfam; PF00229; INF; 1.
DR   PRINTS; PR01234; INFNCROSISF.
DR   ProDom; PD002012; INF_fam; 1.
DR   SMART; SM00207; INF; 1.
DR   PROSITE; PS00251; INF_1; 1.
DR   PROSITE; PS50049; INF_2; 1.
KW   Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal; Multigene
FT   CHAIN         1    208       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 6, MEMBRANE FORM.
FT   CHAIN       151    242       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT   DOMAIN        1     84       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     85    105       TYPE II MEMBRANE PROTEIN
FT                                (POTENTIAL).
FT   DOMAIN      106    242       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN        4     7       PRO-RICH.
FT   DOMAIN       45    54       HYDROPHOBIC.
FT   SITE        135    136       CLEAVAGE (BY SIMILARITY).
FT   DISULFID    203    241       POTENTIAL.
FT   CARBOHYD    185    185       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    201    201       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    231    231       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT      5      5       P -> L (IN REF. 4).
FT   CONFLICT     57     57       S -> P (IN REF. 2).
SQ   SEQUENCE   242 AA;  [illegible] MW;  [illegible] CRC64;
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  Query Match             2.6%;  Score 8;  DB 1;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      307 RETPPLPE 314
            ||||||||
Db       62 RETPPLPE 69


RESULT 15
PGK_ESVCB
ID   PGK_ESVCB      STANDARD;      PRT:   545 AA.
AC   P06514;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tyrosine protein kinase transforming protein PGK (EC ...).
GN   V-PGK OR SRC 2.
OS   Feline sarcoma virus (strain Snyder-Theilen).
OC   Viruses; Retroid viruses; Retroviridae; Mammalian type ... Retroviruses.
OX   NCBI_TaxID=11775;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84095751; PubMed=6418414;
RA   Nakamura S., Robbins K.C., Reddy E.P.;
RT   "Gene product of v-fps oncogene: hybrid protein containing a portion of
RT   actin and a tyrosine specific protein kinase.";
RL   Science 223:63-66(1984).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- FUNCTION: ... is essential ... stimulation of A-DAT ...
CC       ACTIVITIES.
CC   -!- SUBCELLULAR LOCATION: ... THE CYTOPLASMIC ... OF ... TYPE KINASES (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC   ---------- ---------- ---------- ----------
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ID EMBL; X96684; SAA96684; PRT; 892 AA.
AC Q96KY5; Q96RY0; Q9BZB3;
DT 25-JUN-2002 (Rel. 41, Created)
DT 25-JUN-2002 (Rel. 41, Last sequence update)
DT 25-JUN-2002 (Rel. 41, Last annotation update)
DE Hypermethylated in cancer 1 protein (Hic-1).
GN HIC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
RC STRAIN 129/SV; TISSUE=Liver;
RX MEDLINE=99297644; PubMed=10072443;
RA Grimm C., Spaetle R., Schmid E.E., Adler I.D., Aubele M.;
RA Schughart K., Graw J.;
RT "Isolation and embryonic expression of the mouse, mapped proximal to the
RT homeobox A1 locus, a candidate gene for the Mi-1 breast cancer antigen.";
RL Hum. Mol. Genet. 8:1097-1105(1999).
RN [2]
RP SEQUENCE FROM N.A., DISEASE, AND TISSUE SPECIFICITY.

RX MEDLINE=20122275; PubMed=10655551;
RA Carter M.G., Johns M.A., Zeng X., Zhou L., Zink M.C., Mankowski J.L.,
RA Donahue R.N., Baylin S.B.;
RT "Mice deficient in the candidate tumor suppressor gene Hic1 exhibit
RT developmental defects of structures affected in the Miller-Dieker
RT syndrome.";
RL Hum. Mol. Genet. 9:413-419(2000).
RN [3]
RP SEQUENCE OF 179-338 FROM N.A.
RC STRAIN 129/SV; TISSUE=Liver;
RX MEDLINE=99297644; PubMed=10072443;
RA Grimm C., Spaetle R., Schmid E.E., Adler I.D., Aubele M.;
RA Schughart K., Graw J.;
RT "Isolation and embryonic expression of the mouse, mapped proximal to the
RT homeobox A1 locus, a candidate gene for the Mi-1 breast cancer antigen.";
RL Hum. Mol. Genet. 8:1097-1105(1999).
CC -!- FUNCTION: Putative transcription factor. May act as a tumor
CC suppressor. May be involved in development of head, face, limb
CC and ventral body wall.
CC -!- SUBUNIT: Interacts with CTBP (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- ALTERNATIVE PRODUCTS: A number of isoforms may be produced by
CC alternative splicing.
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed with highest levels in
CC heart and lung.
CC -!- DEVELOPMENTAL STAGE: Expression is first detected in the embryo
CC after 9 days post coitum. In the embryo, expression is found in
CC restricted regions of somite derivatives, limb anlagen, and cranio-
CC facial mesenchyme. In the fetus, it is additionally expressed in
CC mesenchymes apposed to precartilaginous condensations, at bone
CC interfaces to budding epithelia of inner organs, and weakly in
CC muscles.
CC -!- DISEASE: Defects in HIC1 are the cause of perinatal death with
CC serious developmental anomalies, including arrest, exencephaly,
CC cleft palate, omphalocoele, craniofacial and limb anomalies.
CC -!- SIMILARITY: BELONGS TO THE KRUPPEL FAMILY OF C2H2 TYPE ZINC
CC FINGER PROTEINS, BTB TRANSCRIPTION FACTORS SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC -!- SIMILARITY: CONTAINS 5 C2H2 TYPE ZINC FINGERS.

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DR EMBL; AF036184; AAC80654.1; -.
DR EMBL; AF036582; AAC80655.1; -.
DR EMBL; AJ132661; CAB44466.1; -.
DR PDB; 1HIC; 14-JUL-00.
DR MGD; MGI:1346010; Hic1.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR000822; Znf_C2H2.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00096; zf-C2H2; 5.
DR Prodom; PD000000; Znf_C2H2; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00355; ZnF_C2H2; 5.
DR PROSITE; PS50097; BTB; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
KW Multigene family; Nuclear protein; Transcription regulation;
KW DNA-binding; Zinc-finger; Metal-binding; Repeat;
KW Developmental protein; Alternative splicing.
FT DOMAIN 1 174 APC/PIR/GLY RICH.
FT DOMAIN 206 269 BTB.
FT DOMAIN 271 278 POLY ALA.
FT DOMAIN 315 320 POLY GLY.
FT DOMAIN 454 458 POLY-PRO.
FT DOMAIN 596 777 ZINC FINGERS.
FT ZN_FING 596 624 C2H2 TYPE.

```
ID   ZN_FING     STANDARD;      PRT;   ### AA.
AC   P#####;
DT   ##-###-#### (Rel. ##, Created)
DT   ##-###-#### (Rel. ##, Last sequence update)
DT   ##-###-#### (Rel. ##, Last annotation update)
DE   Hypothetical protein AF0149.
GN   AF0149.
OS   Archaeoglobus fulgidus.
OC   Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC   Archaeoglobaceae; Archaeoglobus.
OX   NCBI_TaxID=#####;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DSM ####### / ### ### ### ;
RX   MEDLINE=########; PubMed=########;
RA   Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA   Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA   Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA   Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA   Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA   Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA   Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA   Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA   Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA   Venter J.C.;
RT   "The complete genome sequence of the hyperthermophilic, sulfate-
RT   reducing archaeon Archaeoglobus fulgidus.";
RL   Nature 390:364-370(1997).
CC   !! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------
DR   EMBL; AE001096; AAB90108.1; -.
DR   PIR; A64149; A64149; -.
KW   Hypothetical protein; Transmembrane; Complete proteome.
FT   TRANSMEM      4     20       POTENTIAL.
FT   TRANSMEM     27     49       POTENTIAL.
FT   TRANSMEM     57     81       POTENTIAL.
SQ   SEQUENCE   84 AA;  ##### MW;  ######## ######## CRC64;

  Query Match             ##.#%;  Score ##;  DB #;  Length ##;
  Best Local Similarity   ##.#%;  Pred. No. ###;
  Matches   ##;  Conservative   ##;  Mismatches   ##;  Indels   ##;  Gaps   ##;

Qy      ### LLLLAIL 246
            |||||||
Db       ## LLLAIL 88

RESULT 2
YI44_ARCFU
ID   YI44_ARCFU     STANDARD;      PRT;   ### AA.
AC   O#####;
DT   ##-###-#### (Rel. ##, Created)
DT   ##-###-#### (Rel. ##, Last sequence update)
DT   ##-###-#### (Rel. ##, Last annotation update)
DE   Hypothetical protein AF0149.
GN   AF0744.
OS   Archaeoglobus fulgidus.
OC   Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC   Archaeoglobaceae; Archaeoglobus.
OX   NCBI_TaxID=#####;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DSM ####### / ### ### ### ;
RX   MEDLINE=########; PubMed=########;
RA   Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA   Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA   Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA   Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA   Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA   Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA   Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA   Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA   Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA   Venter J.C.;
RT   "The complete genome sequence of the hyperthermophilic, sulfate-
RT   reducing archaeon Archaeoglobus fulgidus.";
RL   Nature 390:364-370(1997).
CC   !! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -------------------------------------------------------------------
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CC   -------------------------------------------------------------------
DR   EMBL; AE001096; AAB90108.1; -.
DR   PIR; AF0149; -.
KW   Hypothetical protein; Transmembrane; Complete proteome.
FT   TRANSMEM      4     20       POTENTIAL.
FT   TRANSMEM     27     49       POTENTIAL.
FT   TRANSMEM     57     81       POTENTIAL.
SQ   SEQUENCE   84 AA;  ##### MW;  ######## ######## CRC64;

  Query Match             ##.#%;  Score ##;  DB #;  Length ##;
  Best Local Similarity   ##.#%;  Pred. No. ###;
  Matches   ##;  Conservative   ##;  Mismatches   ##;  Indels   ##;  Gaps   ##;

Qy      ### LLLLAIL 246
            |||||||
Db       ## LLLAIL 88

RESULT 3
RK25_HEA
ID   RK25_HEA       STANDARD;      PRT;   ### AA.
AC   P#####;
DT   ##-###-#### (Rel. ##, Created)
DT   ##-###-#### (Rel. ##, Last sequence update)
DT   ##-###-#### (Rel. ##, Last annotation update)
DE   50S ribosomal protein L25, chloroplast precursor.
OS   Pisum sativum (Garden pea).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; tracheophytes;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
OX   NCBI_TaxID=####;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Little Marvel; TISSUE=Seedling;
RX   MEDLINE=########; PubMed=########;
RA   Gantt J.S.;
RT   "Nucleotide sequences of cDNAs encoding four ribosomal protein genes
RT   plastid ribosomal proteins.";
RL   Curr. Genet. ##:###-###(####).
CC   -!- ---
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------
DR   EMBL; X#####; CAA#####.1; -.
DR   PIR; S#####; R5PM25.
KW   Ribosomal protein; Chloroplast; Transit peptide.
FT   SIGNAL        1     ##       POTENTIAL.
FT   CHAIN        ##    ###       50S RIBOSOMAL PROTEIN L25.
SQ   SEQUENCE   ### AA;  ##### MW;  ######## ######## CRC64;

  Query Match             ##.#%;  Score ##;  DB #;  Length ##;
  Best Local Similarity   ##.#%;  Pred. No. ##;
  Matches   ##;  Conservative   ##;  Mismatches   ##;  Indels   ##;  Gaps   ##;

Qy      ### LLLPLPP 414
            || |||
Db       ## LLPLPP 80

RESULT 17
RISB_CLOAB
ID   RISB_CLOAB     STANDARD;      PRT;   ### AA.
AC   Q#####;
DT   ##-JUN-2002 (Rel. ##, Created)
DT   ##-JUN-2002 (Rel. ##, Last sequence update)
DT   ##-JUN-2002 (Rel. ##, Last annotation update)
DE   6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
DE   (Lumazine synthase) (Riboflavin synthase beta chain).
GN   RIBH OR CAC0593.
OS   Clostridium acetobutylicum.
OC   bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=####;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC ###### / ### ### / VKM B-####;
RX   MEDLINE=########; PubMed=########;
RA   Nolling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA   Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA   Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA   Bennett G.N., Koonin E.V., Smith D.R.;
RT   "Genome sequence and comparative analysis of the solvent-producing
RT   bacterium Clostridium acetobutylicum.";
RL   J. Bacteriol. ###:####-####(####).
```

```
CC   !  FUNCTION: Riboflavin synthase is a bifunctional enzyme complex
CC      catalyzing the formation of riboflavin from 5-amino-6-(5'-
CC      ribitylamino)-2,4(1H,3H)-pyrimidinedione and 3,4-dihydroxy-2-
CC      butanone 4-phosphate via 6,7-dimethyl-8-ribityllumazine. Riboflavin
CC      catalyzes the condensation of 5-amino-6-(5'-ribitylamino)-
CC      2,4(1H,3H)-pyrimidinedione with 3,4-dihydroxy-2-butanone 4-
CC      phosphate yielding 6,7-dimethyl-8-ribityllumazine (by similarity).
CC   !  CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-ribityl)lumazine =
CC      riboflavin + 4 (5-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
CC   !  PATHWAY: Riboflavin biosynthesis; last step.
CC   !  SIMILARITY: BELONGS TO THE DMRL SYNTHASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE000512; AAK76521.1; -.
DR   PIR; G90175; G90175.
DR   InterPro; IPR002180; DMRL_synthase.
DR   Pfam; PF00885; DMRL_synthase; 1.
DR   TIGRFAMs; TIGR00114; ribB; 1.
KW   Riboflavin biosynthesis; Transferase; Complete proteome.
SQ   SEQUENCE   155 AA;  16480 MW;  0F1A4B5E7 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 155;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      275 EPLSAVI 281
            |||||||
Db      76 EPLSAVI 82

RESULT 18
RISB_SYNY3
ID   RISB_SYNY3     STANDARD;      PRT;   154 AA.
AC   P73547;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
DE   (Lumazine synthase) (Riboflavin synthase beta chain).
GN   RIBB OR SLL1284.
OS   Synechocystis sp. (strain PCC 6803).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX   NCBI_TaxID=1148;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97061201; PubMed=8955243;
RA   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA   Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
RA   Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA   Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA   Yamada M., Yasuda M., Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT   entire genome and assignment of potential protein-coding regions.";
RL   DNA Res. 3:109-136(1996).
CC   !  FUNCTION: Riboflavin synthase is a bifunctional enzyme complex
CC      catalyzing the formation of riboflavin from 5-amino-6-(5'-
CC      ribitylamino)-2,4(1H,3H)-pyrimidinedione and 3,4-dihydroxy-2-
CC      butanone 4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit
CC      catalyzes the condensation of 5-amino-6-(5'-ribitylamino)-
CC      2,4(1H,3H)-pyrimidinedione with 3,4-dihydroxy-2-butanone 4-
CC      phosphate yielding 6,7-dimethyl-8-lumazine (by similarity).
CC   !  CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-ribityl)lumazine =
CC      riboflavin + 4 (5-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
CC   !  PATHWAY: Riboflavin biosynthesis; last step.
CC   !  SIMILARITY: BELONGS TO THE DMRL SYNTHASE FAMILY.
CC   ---------------------------------------------------------------------
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RESULT 1
ID   EMBL; DT=07-JUL-1993 (Rel. 37, Created)
DE   ESSP; P(1)98; IFVV.
DE   Interleu; Leu-Val-Pro; EMBL_synthase.
DE   Pfam; PF00486; EMBL_synthase; 1.
DE   Prosom; PS_00464; EMBL_synthase; 1.
DE   INTERPRO; IPR001144; EMBL; 1.
KW   Interleukin biosynthesis; Transferase; Angiotensin-converting enzyme.
SQ   SEQUENCE   154 AA;  17617 MW;  4B1F2F4D7C8CA0C5 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 154;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     27 IPLSAVI 279
           |||||||
Db     82 IPLSAVI 88


RESULT 2
IBPI_ARATH
ID   IBPI_ARATH     STANDARD;      PRT;   172 AA.
AC   Q42XP8;
DT   15-OCT-2001 (Rel. 39, Created)
DT   15-OCT-2001 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Chloroplast F-type 1, chloroplast precursor (IPX ).
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Vorderwulbecke T., Meyer Y.;
RT   "Characterisation of the Arabidopsis thaliana [illegible].";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Participates in various redox reactions involving
CC       reversible oxidation of the active center dithiol, forming
CC       the F core is known to activate a number of enzymes [illegible]
CC       photosynthetic carbon cycle (by similarity).
CC   -!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY, [illegible].
CC   ---------- ---------- ---------- ----------
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CC   ---------- ---------- ---------- ----------
DR   EMBL; AF244386; AAG45011.1; -.
DR   HSSP; P35906; 1AIP.
DR   InterPro; IPR001144; IbCoord.
DR   Pfam; PF00486; thioredx; 1.
DR   PRINTS; PR00421; THIOREDOXIN.
DR   PROSITE; PS00194; THIOREDOXIN; 1.
KW   Redox active center; Electron transport; Chloroplast; Transit peptide;
KW   Multigene family.
FT   TRANSIT       1      2       CHLOROPLAST (POTENTIAL).
FT   CHAIN         3    170       THIOREDOXIN F [YE].
FT   DISULFID     89    104       REDOX-ACTIVE (BY SIMILARITY).
SQ   SEQUENCE   170 AA;  19451 MW;  7B45F1FF89250B8A CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 SFSIAL 8
          |||||| |
Db      8 SFSFAL 14


RESULT 21
ORF_SHEEP
ID   ORF_SHEEP      STANDARD;      PRT;   197 AA.
AC   P01142;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Corticotherin precursor (Corticotropin releasing factor) (Endorphetherin)
DE   (Corticotropin releasing hormone) (Endorphetherin).
GN   ORF.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Pecora; Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE 83115025; PubMed 6601215;
RA   Furutani Y., Morimoto Y., Shibahara S., Noda M., Takahashi H.,
RA   Hirose T., Asai M., Inayama S., Hayashida H., Miyata T., Numa S.;
RT   "Cloning and sequence analysis of cDNA for ovine
RT   corticotropin releasing factor precursor.";
RL   Nature 301:537-540(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE 86186085; PubMed 3007587;
RA   Roche P.J., Gruetzmann R.J., Pressey R.I., Hexham J.M., Tervit J.R.;
RT   "Nucleotide sequence of the open reading for ovine corticotropin
RT   releasing factor and regulation of its mRNA levels by
RT   glucocorticoids.";
RL   Gene 71:423-431(1988).
RN   [3]
RP   SEQUENCE OF 148-188.
RX   MEDLINE 82208246; PubMed 6279771;
RA   Spiess J., Rivier J., Rivier C., Vale W.;
RT   "Primary structure of corticotropin-releasing factor-41 from
RT   hypothalamus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:6517-6521(1981).
RN   [4]
RP   SEQUENCE OF 148-188, AND SYNTHESIS OF 148-188.
RX   MEDLINE 81274819; PubMed 6267679;
RA   Vale W., Spiess J., Rivier C., Rivier J.;
RT   "Characterization of a 41 residue ovine hypothalamic peptide that
RT   stimulates secretion of corticotropin and beta-endorphin.";
RL   Science 213:1394-1397(1981).
RN   [5]
RP   SEQUENCE OF 148-188.
RX   MEDLINE 89196626; PubMed 2537592;
RA   Auddya I., Hollander C.S., Schlessinger D.H., Hatcher-Solis B.;
RT   "Structural characterization and localization of
RT   corticotropin releasing factor in testis.";
RL   Biochim. Biophys. Acta 1007:116(1989).
CC   -!- FUNCTION: THIS GENE MAY ENCODE A BIFUNCTIONAL PROTEIN WHICH
CC       POSSESSES BOTH A CORTICOTROPIN RELEASING HORMONE BINDING
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN RELEASING
CC       FACTOR FAMILY OF PEPTIDES.
CC   ---------- ---------- ---------- ----------
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CC   ---------- ---------- ---------- ----------
DR   EMBL; J00593; AAA31011.1; -.
DR   EMBL; M12853; AAA31013.1; -.
DR   PIR; JS0330; JS0330.
DR   PIR; S19426; S19426.
DR   InterPro; IPR000187; Corticotr_releas.
DR   InterPro; IPR001870; Sauvagine.
```

```
DR   Pfam; PF00412; GRP; 2.
DR   Prosite; PS00307; Glycocitin_PPI; 1.
DR   SMART; SM00649; GRP; 1.
DR   PROSITE; PS00514; GRP; 1.
KW   Hormone; Amidation; Hypothalamus; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     21       PROBABLE.
FT   PROPEP       22     47
FT   PEPTIDE      48    108       GONADOTROPIN-RELEASING HORMONE II.
FT   MOD_RES      48     48       AMIDATION (BY SIMILARITY).
FT   CONFLICT     52     52       K -> E (IN REF. 2).
SQ   SEQUENCE   108 AA;  12072 MW;  B5C0B8B7EB852B0EE CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     255 ISPASIA 261
           |||||||
Db     120 ISPASIA 126


RESULT 22
EHNB_BPBMI
ID   PHNB_BPBME     STANDARD;      PRT:   256 AA.
AC   Q63908;
DT   01-MAY-2000 (Rel. 39, Created)
DT   01-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2004 (Rel. 43, Last annotation update)
DE   EhnB protein.
GN   EHNB OR ERIL2 OR SMB20760.
OS   Rhizobium meliloti (Sinorhizobium meliloti).
OC   Plasmid pSymB (megaplasmid 2).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Sinorhizobium.
OX   NCBI_TaxID=382;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN 1021;
RA   McLean P.A., Lin C.M., Sookdeo C.C., Cannon F.C.;
RT   "Characterization of a gene cluster involved in glyphosate and";
RT   glyphosate and other phosphonates in Rhizobium meliloti.";
RL   Submitted (NOV 1992) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN 1021;
RX   MEDLINE=21590508; PubMed=11483414;
RA   Eitan I.M., Wexler S., Wolf K., Bourgeois J., Clark I.,
RA   Verhoeffen E.L., Hernandez Lucas I., Becker A., Cowie A., Gyorgypal ...
RA   Goldfine B., Puehler A.;
RT   "The complete sequence of the 1,683 kb pSymB megaplasmid from the N...
RT   fixing endosymbiont Sinorhizobium meliloti.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
CC   -!- FUNCTION: RELEASES AN OPERON INVOLVED IN UTILIZATION
CC       GLYPHOSATE AND OTHER PHOSPHONATES.
CC   -----
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CC   -----
DR   EMBL; M90356; AAA26451.1;  -.
DR   EMBL; AL591688; CAC47241.1;  -.
KW   Alkylphosphonate uptake; Plasmid; Complete proteome.
SQ   SEQUENCE   256 AA;  27125 MW;  4CE648E5ADFAFC1 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     139 GEGPAL 145
           |||||||
Db     111 GEGPAL 117


RESULT 23
YBL7_YEAST
ID   YBL7_YEAST     STANDARD;      PRT:   215 AA.
AC   P38212;
DT   01-OCT-1994 (Rel. 29, Created)
DT   01-OCT-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical 23.5 kDa protein in CAT1-DCW2 intergenic region.
GN   YBR007W OR YBR0111.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC   Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN S288C;
RA   Dujon B., Sussenbuter H., Obermaier B., Lazzaroni E.;
RL   Submitted (AUG 1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO YEAST SSB1.
CC   -----
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CC   -----
DR   EMBL; Z35674; CAA84041.1;  -.
DR   PIR; S45857; S45857.
DR   SGD; S0000209; YBR007W.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM     40     62       POTENTIAL.
SQ   SEQUENCE   215 AA;  23886 MW;  0741F6B82C16B1ED CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     277 AVILIL 283
           ||||||
Db      71 AVILIL 77


RESULT 24
MLO_LINUS
ID   MLO_LINUS      STANDARD;      PRT:   217 AA.
AC   P93785;
DT   15-DEC-1998 (Rel. 36, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Mlo-like protein (Fragment).
OS   Linum usitatissimum (Flax) (Linseed).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   Eurosids I; Malpighiales; Linaceae; Linum.
OX   NCBI_TaxID=4006;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN cv. Antares; TISSUE=Cotyledon;
RA   McKay S.J.;
RL   Submitted (APR 1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC   -----
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DR   EMBL; D90899; BAA16582.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   233 AA;  26455 MW;  D4D5D4A0F8A3F273 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 233;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      10 VIAAHS 15
           |||||
Db     220 VIAAHS 225


RESULT 25
Y581_SYNY3
ID   Y581_SYNY3     STANDARD;      PRT:   233 AA.
AC   P74284;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ycf54-like protein.
GN   SLL0558.
OS   Synechocystis sp. (strain PCC 6803).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX   NCBI_TaxID=1148;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96387181; PubMed=8905231;
RA   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA   Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
RA   Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA   Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA   Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT   entire genome and assignment of potential protein-coding regions.";
RL   DNA Res. 3:109-136(1996).
CC   -!- SIMILARITY: BELONGS TO THE YCF54 FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D90899; BAA16582.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   233 AA;  26455 MW;  D4D5D4A0F8A3F273 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 233;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      10 VIAAHS 15
           |||||
Db     220 VIAAHS 225


RESULT 26
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ID   IPIS_SALEN
ID   IPIS_SALEN     STANDARD;      PRT:   254 AA.
AC   Q7Z5Z6; Q6US70; Q9KIY1;
DT   30-MAY-2003 (Rel. 41, Created)
DT   16-OCT-2003 (Rel. 42, Last sequence update)
DT   16-OCT-2003 (Rel. 42, Last annotation update)
DE   Triosephosphate isomerase (EC 5.3.1.1) (TIM).
GN   TPIA OR ZH1458 OR VNG1026G.
OS   Halobacterium salinarum (Halobacterium halobium).
OC   Archaea; Euryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae;
OC   Halobacterium.
OX   NCBI_TaxID=2242;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NRC-1;
RX   MEDLINE=20150215; PubMed=10944509;
RA   Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D.,
RA   Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S.,
RA   Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B.,
RA   Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G.,
RA   Jones P.E., Klingenberg M., Ambulos N., Facciotti M.T., Hood L.;
RT   "Genome sequence of Halobacterium species NRC-1.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 43870 / DSM 3754 / JCM 8978 / NBRC 102226 / NRC-1;
RX   MEDLINE=21218340; PubMed=11259648;
RA   Kawashima T., Amano N., Koike H., Makino S., Higuchi S.,
RA   Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA   Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Morimoto H.;
RT   "Archaeal adaptation to higher temperatures revealed by genomic
RT   sequence of Thermoplasma volcanium.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 29133 / DSM 3696 / JCM 8854 / NBRC 100826;
RX   MEDLINE=20450349; PubMed=11076862;
RA   Shinkai A., Hirakawa H., Kimata-Ariga Y., Sakamoto K., Yamamoto I.,
RA   Shiba T., Ishii K., Hattori M., Kihara S., Nakamura S.;
RT   "Comparison of whole gene sequences of Thermoplasma prototype TPV8
RT   from Japan and TWEU2 from USA.";
RL   Nucleic Acids Res. 28:4317-4324(2000).
CC   -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = dihydroxyacetone
CC       phosphate.
CC   -!- PATHWAY: Carbohydrate metabolism; glycolysis; D-glyceraldehyde 3-
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AE004987; AAG19423.1; -.
DR   EMBL; AF096288; AAD12416.1; -.
DR   PIR; G84510; G84510.
DR   HSSP; P36204; 1TRE.
DR   PROT-2DPAGE; Q9Z6J6; -.
DR   TIGR; CP0786; -.
DR   InterPro; IPR000652; Triosephos_isomerase.
DR   Pfam; PF00121; TIM; 1.
DR   ProDom; PD001005; Triosephos_isomerase; 1.
DR   TIGRFAMs; TIGR00419; tim; 1.
DR   PROSITE; PS00171; TIM; 1.
KW   Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW   Pentose shunt; Complete proteome.
FT   ACT_SITE     99     99       BY SIMILARITY.
FT   ACT_SITE    169    169       BY SIMILARITY.
FT   CONFLICT     96     96       M -> V (IN REF. 1).
FT   CONFLICT    112    112       P -> L (IN REF. 3).
SQ   SEQUENCE   254 AA;  27703 MW;  E07B0548B7AE7F98 CRC64;
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  Query Match             21.1%;  Score 7;  DB 1;  Length 279;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      25 PSEATAE 29
           |||||||
Db     200 PSEATAE 204


RESULT 27
INF6_CERTE
ID   INF6_CERTE     STANDARD;      PRT:   283 AA.
AC   Q08BN1;
DT   05-JUN-2002 (Rel. 41, Created)
DT   05-JUN-2002 (Rel. 41, Last sequence update)
DT   05-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE   (CD95 protein).
GN   INF6F6 OR FASL OR CD95L.
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
OC   Cercocebus.
OX   NCBI_TaxID=9535;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocyte;
RX   MEDLINE=21449719; PubMed=11493595;
RA   Viejo-Borbolla A., Martin-Villa J.M., Kuroda M.J., Marcos C.Y.,
RA   Regueiro J.R., Wakisaka A., Arnaiz-Villena A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas ligand and costimulatory molecules.";
RL   Immunogenetics 53:415-428(2001).
CC   -!- FUNCTION: Cytokine that binds to INFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell-mediated apoptosis and in T cell development.
CC       INFRSF6/FAS mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen stimulated activation of mature
CC       T cells, or both. Binding to the decoy receptor INFRSF6B/DcR3
CC       modulates its effects (By similarity).
CC   -!- SUBUNIT: Homotrimer (Probable).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (By
CC       similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
DR   EMBL; AF344847; AAK37406.1; -.
DR   HSSP; P48023; 4ISV.
DR   InterPro; IPR008983; INF_like.
DR   InterPro; IPR006052; INF_family.
DR   Pfam; PF00229; INF; 1.
DR   PRINTS; PR01234; INFNCROSISFT.
DR   ProDom; PD000204; INF_like; 1.
DR   PROSITE; PS50049; INF_1; 1.
DR   PROSITE; PS50050; INF_2; 1.
KW   Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT   CHAIN         1    200       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 6, MEMBRANE FORM.
FT   CHAIN       129    200       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT   DOMAIN        1     80       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     81    101       SIGNAL ANCHOR (TYPE II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN      102    200       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN        4     44       POR REGION.
FT   DOMAIN       47     64       POLY PRO.
FT   SITE        128    129       CLEAVAGE (BY SIMILARITY).
FT   DISULFID    201    232       POTENTIAL.
FT   CARBOHYD    183    183       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    249    249       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    259    259       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   280 AA;  31407 MW;  7A7EAF000787C0C8 CRC64;

  Query Match             21.1%;  Score 7;  DB 1;  Length 280;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      25 PSEATAE 29
           |||||||
Db      63 PSEATAE 69


RESULT 28
INF6_HUMAN
ID   INF6_HUMAN     STANDARD;      PRT:   281 AA.
AC   P48023; Q96BZ5;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE   (Apoptosis antigen ligand) (APTL) (CD178 antigen).
GN   INFSF6 OR FASLG OR APTL1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=95185741; PubMed=7528780;
RA   Anderson M.;
RT   "Fas ligand mediates activation-induced cell death in human T
RT   lymphocytes.";
RL   J. Exp. Med. 181:71-77(1995).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=95127560; PubMed=7626147;
RA   Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT   "Human Fas ligand: gene structure, chromosomal location and species
RT   specificity.";
RL   Int. Immunol. 6:1567-1574(1994).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Schneider-Brachert W., Krippner-Heidenreich A., Ruehl H.,
RA   Siegmund D., Kabelitz D., Lackmann M.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=95071456; PubMed=7964512;
RA   Mita E., Hayashi N., Iio S., Takehara T., Hiramatsu T., Kasahara A.,
RA   Fusamoto H., Kamada T.;
RT   "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT   infection.";
RL   Biochem. Biophys. Res. Commun. 204:798-804(1994).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Leukocyte;
RA   Zeytun A., Nagarkatti M., Nagarkatti P.S.;
RT   "Isolation and characterization of a new naturally occurring variant of
RT   human Fas ligand that is expressed only in membrane bound form.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Wilkinson J.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Blood;
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RA   Stanislovaitis P.;
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast;
RA   Matsushima M., Nikinishi Y., Ohba Y.;
RT   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   CHARACTERIZATION, AND MUTAGENESIS OF GLU-[illegible].
RX   PubMed=9228050;
RA   Schneider P., Bodmer J.-L., Becker N., Mattmann C., Holler N.,
RA   Tschopp J., Piguet P.-F.;
RT   "Characterization of Fas (Apo-1, CD95) Fas-ligand interaction.";
RL   J. Biol. Chem. 272:18827-18833(1997).
RN   [6]
RP   PROCESSING.
RX   PubMed=9127966;
RA   Tanaka M., Itai T., Adachi M., Nagata S.;
RT   "Downregulation of Fas ligand by shedding.";
RL   Nat. Med. 3:416-420(1998).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in the regulation of normal
CC       TNFRSF6/FAS mediated apoptosis may have a role in the pathogenesis
CC       of peripheral tolerance, in the antigen stimulated suppression of
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       antagonizes its effects.
CC   -!- SUBUNIT: HOMOTRIMER (PROBABLE).
CC   -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE ALSO
CC       FOUND IN THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FROM THE CELL
CC       SURFACE.
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (short form) and 2
CC       are produced by alternative splicing.
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing.
CC   -!- DISEASE: Defects in TNFSF6 are a cause of autoimmune
CC       lymphoproliferative syndrome (ALPS), also known as Canale-Smith
CC       syndrome (CSS), a childhood syndrome characterized by chronic non-
CC       malignant lymphoproliferation, autoimmune hemolytic anemia
CC       and thrombocytopenia. [illegible] type II diabetes mellitus
CC       spontaneously.
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   -!- DATABASE: NAME=CD95; NOTE=FAS antigen entry;
CC       URL="[illegible]".
CC   ---------- [illegible] ---------- [illegible] ----------
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CC   ---------- [illegible] ----------
DR   EMBL; X83493; CAA58474.1; -.
DR   EMBL; U83245; AAB39071.1; -.
DR   EMBL; D12021; AAA59424.1; -.
DR   EMBL; L07932; AAA59423.1; -.
DR   EMBL; AF028857; AAC08717.1; -.
DR   EMBL; Z46975; CAA86124.1; -.
DR   EMBL; U60975_2; AAB17502.1; -.
DR   EMBL; AB017503; BAA24742.1; -.
DR   PIR; I57175; I57175.
DR   GenRew; HGNC:11936; TNFSF6.
DR   MIM; 134637; -.
DR   MIM; 601859; -.
DR   InterPro; IPR008983; TNF_like.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   Prosite; PS00422; TNF_1; 1.
DR   SMART; SM00207; TNF; 1.
DR   ProDom; PD000561; TNF; 1.
DR   ProSite; PS50049; TNF_2; 1.
KW   Cytokine; Apoptosis; Transmembrane; Glycoprotein; Polymorphism;
KW   Alternative splicing; Autoimmune disease.
FT   DOMAIN          1     [illegible]     CYTOPLASMIC (POTENTIAL).
FT                                         MEMBRANE; MEMBRANE FORM.
FT   DOMAIN        [illegible]  26.        EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      [illegible]  [illegible]  SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT                                         (POTENTIAL).
FT   DOMAIN        [illegible]  [illegible]  EXTRACELLULAR (POTENTIAL).
FT   DOMAIN          4     71.             TNF-LIKE.
FT   DOMAIN         45     65              LOOP.
FT   SITE          129     130             CLEAVAGE.
FT   DISULFID      202     233             POTENTIAL.
FT   CARBOHYD      154     154             N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      250     250             N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      260     260             N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC      117     130             [illegible]
FT                                         [illegible]
FT   VARSPLIC      128     208             MISSING (IN ISOFORM 2).
FT   MUTAGEN       206     209             [illegible]
FT                                         AND REDUCES CYTOTOXICITY MORE THAN A
FT                                         HUNDREDFOLD.
FT   MUTAGEN       218     219             Y->F,R: LOWERS BINDING TO TNFRSF AND
FT                                         ABOLISHES CYTOTOXICITY.
FT   MUTAGEN       275     279             [illegible] ABOLISHES BINDING TO TNFRSF AND
FT                                         CYTOTOXICITY.
SQ   SEQUENCE   281 AA;  [illegible] MW;  AA0A11C5B24E2B8B CRC64;

  Query Match             [illegible]%;  Score 7;  DB 1;  Length 281;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      [illegible] PEEPPCP 316
            |||||||
Db        67 PEEPPCP 67


RESULT 29
P'AR_HUMAN
ID   P'AR_HUMAN      [illegible]      [illegible]  281 AA.
AC   P24071; Q15724; Q15727; Q13404; Q13604;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Immunoglobulin alpha Fc receptor precursor (IgA Fc receptor) (CD89
DE   antigen).
GN   P'AR OR CD89.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91379066; PubMed=2258708;
RA   Maliszewski C.R., March C.J., Schoenborn M.A., Gimpel S., Shen L.;
RT   "Expression cloning of a human Fc receptor for IgA.";
RL   J. Exp. Med. 172:1665-1672(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RX   MEDLINE=95465486; PubMed=7636184;
RA   de Wit T.P.M., Morton H.C., Capel P.J.A., van de Winkel J.G.J.;
RT   "Structure of the gene for the human myeloid IgA Fc receptor (CD89).";
RL   J. Immunol. 155:1283-1294(1995).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS A.2 AND A.3).
RC   TISSUE=Alveolar macrophage, and Monocyte;
RX   MEDLINE=96247667; PubMed=8666914;
RA   Patry C., Sibille Y., Vouret-Craviari Y., Mostowy S.,
RT   "Identification of Fc alpha receptor (CD89) as a new constitutively
RT   alternative spliced that are differentially expressed between lung
RT   monocytes and alveolar macrophages.";
RL   J. Immunol. 156:4412-4418(1996)
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RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS B AND B DELTA S2).
RA   van Dijk T.B., Morton H.C., Caldenhoven E., Bracke M.,
RA   [illegible]
RL   Submitted (MAY 1996) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM A.3).
RX   MEDLINE [illegible]; PubMed [illegible];
RA   Pleass R.J., Andrews P.D., Kerr M.A., Woof J.M.;
RT   "Alternative splicing of the human IgA Fc receptor [illegible]
RT   neutrophils and eosinophils.";
RL   Biochem. J. 318:771-777(1996).
RN   [6]
RP   SUBUNITS.
RX   MEDLINE [illegible]; PubMed [illegible];
RA   Pfefferkorn L.C., Yeaman G.R.;
RT   "Association of IgA Fc receptors (Fc alpha R) with Fc [illegible]
RT   gamma 2 subunits in U937 cells. Aggregation induces the [illegible]
RT   phosphorylation of gamma 2.";
RL   J. Immunol. 153:3228-3236(1994).
CC   -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS ALPHA.
CC       MEDIATES SEVERAL FUNCTIONS INCLUDING CYTOKINE PRODUCTION.
CC   -!- SUBUNIT: ASSOCIATES WITH THE FC EPSILON RI GAMMA 2 RECEPTOR
CC       INDUCING TYROSINE PHOSPHORYLATION OF GAMMA 2.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (FORM A) AND [illegible]
CC       (FORM B).
CC   -!- ALTERNATIVE [illegible]
CC       A.3/DELTA2, B AND B DELTA S2, [illegible]
CC   -!- TISSUE SPECIFICITY: DIFFERENTIALLY EXPRESSED BETWEEN [illegible] AND
CC       [illegible]
CC       WHILE ALVEOLAR [illegible] EXPRESS A.1 AND A.2 TRANSCRIPTS;
CC       HOWEVER THEY EXPRESS ONLY ONE [illegible]
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2 TYPE DOMAINS.
CC   -!- DATABASE: NAME [illegible]
CC       WWW="http://[illegible]".
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; X54150; CAA[illegible].1; -.
DR   EMBL; X87767; CAA61[illegible].1; -.
DR   EMBL; X87768; CAA61[illegible].1; JOINED.
DR   EMBL; X877[illegible]; CAA61[illegible].1; JOINED.
DR   EMBL; X87766; CAA61[illegible].1; JOINED.
DR   EMBL; X87765; CAA61[illegible].1; JOINED.
DR   EMBL; U43774; AAC50[illegible].1; -.
DR   EMBL; U43677; AAC50[illegible].1; -.
DR   EMBL; U56236; AAB0[illegible].1; -.
DR   EMBL; U56237; AAB0[illegible].1; -.
DR   EMBL; S6[illegible]; AAD14421.1; -.
DR   PIR; [illegible]; [illegible].
DR   HSSP; P43626; 1NKR.
DR   Genew; HGNC:[illegible]; FCAR.
DR   MIM; 147045; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
KW   Receptor; Glycoprotein; Transmembrane; IgA-binding [illegible]
KW   Immunoglobulin domain; Repeat; Signal; Alternative splicing.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    287       IMMUNOGLOBULIN ALPHA FC RECEPTOR.
FT   DOMAIN       22    227       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    228    246       POTENTIAL.
FT   DOMAIN      247    287       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42    107       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN      1[illegible]    2[illegible]       IG-LIKE C2-TYPE DOMAIN 2.
FT   DISULFID     49    [illegible]       BY SIMILARITY.
FT   DISULFID    146    1[illegible]       BY SIMILARITY.
FT   CARBOHYD     65     65       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     7[illegible]     7[illegible]       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    198    198       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     12     23       MISSING (IN ISOFORM B DELTA S2).
FT   VARSPLIC    121    216       MISSING (IN ISOFORM A.3).
FT   VARSPLIC    1[illegible]    216       MISSING (IN ISOFORM A.2).
FT   VARSPLIC    217    2[illegible]       [illegible]NK
FT                                EASADVALESWSQ[illegible]FARIESVCK [illegible]GEYRPVQ
FT                                [illegible]VWV[illegible]GHRAGI (IN ISOFORM B AND
FT                                ISOFORM B DELTA S2).
SQ   SEQUENCE   287 AA;  [illegible] MW;  A2[illegible] CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 287;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        198 LELVVIG 204
              |||||||
Db        115 LELVVIG 121


RESULT 36
K2S5_HUMAN
ID   K2S5_HUMAN     STANDARD;      PRT;   304 AA.
AC   Q14953;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Killer cell immunoglobulin-like receptor 2DS5 precursor (MHC class I
DE   NK cell receptor) (Natural killer associated transcript 9) (NKAT9).
GN   KIR2DS5 OR NKAT9.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE 96270064; PubMed 8662091;
RA   Doehring C., Samaridis J., Colonna M.;
RT   "Alternatively spliced forms of human killer inhibitory receptors.";
RL   Immunogenetics 44:227-230(1996).
CC   -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC       DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; L76672; AAB[illegible].1; -.
DR   HSSP; P43626; 1NKR.
DR   Genew; HGNC:6337; KIR2DS5.
DR   MIM; 604956; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003650; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00410; IG_like; 2.
KW   Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW   Repeat; Multigene family.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    304       KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT                                2DS5.
FT   DOMAIN       22    245       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    246    264       POTENTIAL.
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FT   DOMAIN       205     354       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       355     377       IT LIKE 2. TYPE 1 MAIN 1.
FT   DOMAIN       378     ???       IT LIKE 2. TYPE 1 MAIN 2.
FT   DISULFID      49     148       BY SIMILARITY.
FT   DISULFID     149     198       BY SIMILARITY.
FT   CARBOHYD      67      67       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      84      84       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     178     178       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     223     223       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   ??? AA;  ?????? MW;  ???????????????? CRC??;

  Query Match          ?.1%;  Score ??;  DB ?;  Length ???;
  Best Local Similarity   ???.?%;  Pred. No. ???;
  Matches    ??;  Conservative    ??;  Mismatches    ??;  Indels    ??;  Gaps    ??;

Qy      ??? ????????? ???

Db      ??? ????????? ???


RESULT 41
'AIB_MOUSE
ID   'AIB_MOUSE      STANDARD;      PRT;   ??? AA.
AC   ?????;
DT   ??-???-????  (Rel. 34, Created)
DT   ??-???-????  (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Cathepsin B precursor (EC ?.?.??.??) (Cathepsin B1) (Cathepsin BA).
GN   CTSB.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95236035; PubMed=7724254;
RA   Labuse W.P., Brown D., Castle J., Zeitlin M.F.;
RT   "IFN-gamma increases cathepsin B mRNA levels in mouse peritoneal macrophages.";
RL   J. Leukoc. Biol. ???:???-???(1995).
RN   [2]
RP   SEQUENCE OF 146-301 FROM N.A., AND TISSUE SPECIFICITY.
RC   STRAIN=C57BL/6; TISSUE=Cartilage;
RX   MEDLINE=96326349; PubMed=8769417;
RA   Sundstrom M., Salminen H., Glumoff V., Kirschke H., Ar   ...
RA   Vuorio E.;
RT   "Cathepsin: expression during skeletal development.";
RL   Biochim. Biophys. Acta 1446:?-?, 46(1996).
CC   -!- FUNCTION: IMPORTANT FOR THE OVERALL DEGRADATION OF ???? ????? IN
CC       LYSOSOMES.
CC   -!- CATALYTIC ACTIVITY: HYDROLYSIS OF PEPTIDES AND ????, ACTIVE
CC       AMINO-PEPTIDASE, AS PEPTIDE SUBSTRATES WITH FREE N-???.
CC   -!- SUBUNIT: COMPOSED OF A HEAVY CHAIN AND A LIGHT CHAIN. ??? ???
CC       ??????? ??? ??????? ??? ????? AND LIGHT CHAIN, ??? ????? ???
CC       HELD TOGETHER BY DISULFIDE BONDS.
CC   -!- SUBCELLULAR LOCATION: Lysosomal.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN
CC       IN NON-SKELETAL TISSUES. LOW LEVELS IN ????? ?? ??????.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; D38119; AAA??????.1;  -.
DR   EMBL; ?1.???; ?AA?????.1;  -.
DR   HSSP; P43487; ????.
DR   MEROPS; C01.???; -.
DR   MGD; MGI:???????; Ctsb.
DR   InterPro; IPR???; Peptidase_C1.
DR   PDB; ????; ??-???-????; Split ???????.
DR   Pfam; PF????; Peptidase_C1; 1.
DR   PRINTS; PR?????; PAPAIN.
DR   ProDom; PD??????; Peptidase_C1; 1.
DR   PROSITE; PS????; THIOL_PROTEASE_CYS; FALSE_NEG.
DR   PROSITE; PS?????; THIOL_PROTEASE_HIS; 1.
DR   PROSITE; PS?????; THIOL_PROTEASE_ASN; 1.
KW   Hydrolase; Thiol protease; Lysosome; Glycoprotein; ??????? S...
FT   SIGNAL       1     ??       POTENTIAL.
FT   PROPEP      ??     ???      ACTIVATION PEPTIDE.
FT   CHAIN       ???    ???      ?-CATHEPSIN B MINICHAIN (BY SIMILARITY).
FT   CHAIN       ???    ???      ?-CATHEPSIN B (BY SIMILARITY).
FT   CHAIN       ???    ??       ?-CATHEPSIN B HEAVY CHAIN (BY SIMILARITY).
FT   CHAIN       ???    ???      ?-CATHEPSIN B LIGHT CHAIN (BY SIMILARITY).
FT   ACT_SITE    ???    ???      BY SIMILARITY.
FT   ACT_SITE    ???    ???      BY SIMILARITY.
FT   ACT_SITE    ???    ???      BY SIMILARITY.
FT   DISULFID    ???    ???      BY SIMILARITY.
FT   DISULFID    ???    ???      BY SIMILARITY.
FT   DISULFID    ???    ???      BY SIMILARITY.
FT   DISULFID    ???    ???      BY SIMILARITY.
FT   CARBOHYD     ??     ?       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     ??     ??      N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    ???    ???      N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT    ???     ??      A -> ? (IN REF. ?).
SQ   SEQUENCE   ??? AA;  ?????? MW;  ???????????????? CRC??;

  Query Match          ?.1%;  Score ??;  DB ?;  Length ???;
  Best Local Similarity   ???.?%;  Pred. No. ???;
  Matches    ??;  Conservative    ??;  Mismatches    ??;  Indels    ??;  Gaps    ??;

Qy      ??? ATALLIV ???
            | | |
Db      ??? TS ATALLIV ???


RESULT 42
'AIB_RAT
ID   'Aim RA.        STANDARD;      PRT;   ??? AA.
AC   P?????;
DT   ??-???-????  (Rel. ??, Created)
DT   ??-???-????  (Rel. ??, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Cathepsin B precursor (EC ?.?.??.??) (Cathepsin B1) (Cathepsin BA).
GN   CTSB.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Kidney;
RX   MEDLINE=????????; PubMed=????????;
RA   Ishidoh K., Imajoh S., Emori Y., Ohno S., Kawasaki H., Mitsui Y.,
RA   Kominami E., Katunuma N., Suzuki K.;
RT   "Molecular cloning and sequencing of cDNA for rat cathepsin B.
RT   Homology in pro peptides regions of cysteine proteinases.";
RL   FEBS Lett. 226:33-37(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=??????; PubMed=????????;
RA   Ishidoh K., Kominami E., Katunuma N., Suzuki K.;
RT   "Gene structure of rat cathepsin B.";
RL   FEBS Lett. 254:103-107(1989).
RN   [3]
RP   SEQUENCE OF 4-??? FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=????????; PubMed=????????;
RA   Qian F., Frankfater A., Mixan B.V., Chan S.J., Steiner D.F.;
RT   "Molecular cloning of rat preprocathepsin B and the expression of
RT   its lysosomal cathepsins in various tissues and in a rat
RT   pancreatic neoplasm.";
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RC   Int. J. Biochem. 22:1457-1464(1990).
RN   [1]
RP   SEQUENCE, 3-111 <<<.
RC   TISSUE=Liver;
RX   MEDLINE=93221054; PubMed=8472365;
RA   Takio K., Towatari T., Katunuma N., Teller D.C., Titani K.;
RT   "Homology of amino acid sequences of rat liver cathepsins B and H
RT   with that of papain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:3666-3670(1983).
CC   -!- FUNCTION: IMP PLAND FOR THE OVERALL ELIMINATION OF PROTEINS IN
CC       LYSOSOMES.
CC   -!- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS WITH BROAD SPECIFICITY FOR
CC       AMINO ACIDS, SIMILAR TO THAT OF PAPAIN.
CC   -!- SUBUNIT: COMPOSED OF A HEAVY CHAIN AND A LIGHT CHAIN.
CC       CHAIN MAY BE GLYCOSYLATED. THE HEAVY AND LIGHT CHAIN ARE
CC       HELD TOGETHER BY DISULFIDE BONDS.
CC   -!- SUBCELLULAR LOCATION: Lysosomal.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
CC   ---------- ----------
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CC   ---------- ----------
DR   EMBL; Y00764; CAA68029.1; -.
DR   EMBL; M94182; AAA36404.1; ALT_INIT.
DR   PIR; S09211; KUHUH.
DR   HSSP; P04843; 1PCI.
DR   MEROPS; C01.034;
DR   InterPro; IPR000668; Peptidase_C1.
DR   InterPro; IPR000169; SH3prot_consite.
DR   Pfam; PF00112; Peptidase_C1; 1.
DR   PRINTS; PR00704; PAPAIN.
DR   Prodom; PD000150; Peptidase_C1; 1.
DR   PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR   PROSITE; PS00640; THIOL_PROTEASE_HIS; 1.
DR   PROSITE; PS00139; THIOL_PROTEASE_ASN; 1.
KW   Hydrolase; Thiol protease; Lysosome; Glycoprotein; Signal; Chain;
FT   SIGNAL       1     20       POTENTIAL.
FT   PROPEP      21     96       ACTIVATION (POTENTIAL).
FT   CHAIN       96    253       CATHEPSIN H MINI CHAIN.
FT   CHAIN      114    333       CATHEPSIN H.
FT   CHAIN      114    297       CATHEPSIN H HEAVY CHAIN.
FT   CHAIN      301    333       CATHEPSIN H LIGHT CHAIN.
FT   ACT_SITE   140    140       BY SIMILARITY.
FT   ACT_SITE   279    279       BY SIMILARITY.
FT   ACT_SITE   299    299       BY SIMILARITY.
FT   DISULFID   100    125       BY SIMILARITY.
FT   DISULFID   136    276       BY SIMILARITY.
FT   DISULFID   170    213       BY SIMILARITY.
FT   DISULFID   270    320       BY SIMILARITY.
FT   CARBOHYD   228    228       N-LINKED (GLCNAC...).
FT   VARIANT    287    287       G -> A.
SQ   SEQUENCE   333 AA;  37434 MW;  7C9E4B2E1AA4B1D0 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 333;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      20 AIAEIV 25
           ||||||
Db     109 AIAEIV 114


RESULT 34
Y04348 MEIFA
ID   Y04348_MEIFA     STANDARD;      PRT:   417 AA.
AC   Q38665;
DT   25-JUL-1996 (Rel. 34, Created)
DT   25-JUL-1996 (Rel. 34, Last sequence update)
DT   15-DEC-1999 (Rel. 38, Last annotation update)
DE   Cazalysin-specific cysteine A (Fragment).
OS   Chlorohydra viridissima (Hydra).
OC   Eukaryota; Metazoa; Cnidaria; Hydrozoa; Endocnida; Anthoathecata;
OC   Hydridae; Chlorohydra.
OX   NCBI_TaxID=6082;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98339815; PubMed=9743665;
RA   Sebastian-Buchte I., Bellmeister S., Herrmann-Breckner I.,
RA   Sebastian H.;
RT   "Presence and expression of Ca2+ cycling in the nematocyte lineage.";
RL   J. Cell Sci. 111:2363-2369(1998).
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC       (MITOSIS) TRANSITION, INTERACTS WITH THE CDC2 AND CDK2 PROTEIN
CC       KINASES TO FORM MPF. G2/M CYCLING ACCOMPLATE SIGNALLING DOPING G2
CC       AND ARE ABSOLUTE REQUIRE FOR MITOSIS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN A SUBFAMILY
```

ID E4_HPV16 STANDARD; PRT; 98 AA.
AC P03126;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Minor capsid protein L2.
GN L2.
OS Human papillomavirus type 16
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94267040; PubMed=8178172;
RA Delius H., Hofmann K.;
RT "Primer directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-32(1994).
CC
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DR EMBL; X74474; CAA52647.1; -.
DR PIR; S36507; S36507.
DR InterPro; IPR000704; Late_L2.
DR Pfam; PF00513; late_protein_L2; 1.
KW Coat protein; Late protein.
FT NON_TER 1 1
SQ SEQUENCE 428 AA; 47655 MW; 05B526157F2B072C DB94;

  Query Match 2.1%; Score 7; DB 1; Length 428;
  Best Local Similarity 100.0%; Pred. No. 1;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 407 KPLPPLP 413
|||||||
Db 422 KPLPPLP 428

RESULT 2
VL2_HPV16 STANDARD; PRT; 473 AA.
AC P06756;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Minor capsid protein L2.
GN L2.
OS Human papillomavirus type 16
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94267040; PubMed=8178172;
RA Delius H., Hofmann K.;
RT "Primer directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-32(1994).
CC
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DR EMBL; X74474; CAA52647.1; -.
DR PIR; S36507; S36507.
DR InterPro; IPR000704; Late_L2.
DR Pfam; PF00513; late_protein_L2; 1.
KW Coat protein; Late protein.
FT NON_TER 473 473
SQ SEQUENCE 473 AA; 52655 MW; 05B526157F2B072C DB94;

  Query Match 2.1%; Score 7; DB 1; Length 473;
  Best Local Similarity 100.0%; Pred. No. 1;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 407 KPLPPLP 413
|||||||
Db 467 KPLPPLP 473

RESULT 3
VL2_HPV16 STANDARD; PRT; 473 AA.
AC P06764;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Minor capsid protein L2.
GN L2.
OS Human papillomavirus type 16
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265565; PubMed=8178172;
RA Delius H., Hofmann K.;
RT "Primer-directed sequencing of human papillomavirus types.";

```
ID   Curr. Sp. Microbiol. Immunol., 186:13-43(1994).
XX                                   ----      ----
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CC
DR   EMBL; X74863; CAA52994.1; -.
DR   PIR; S36530; S36530.
DR   InterPro; IPR000784; Late_L2.
DR   Pfam; PF00715; late protein L2; 1.
KW   Viral protein; Late protein.
SQ   SEQUENCE   464 AA;  51134 MW;  F9858F02551B8A7A CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 464;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      208 IESKELPI 214
            ||||||||
Db      308 IESKELPI 314


RESULT 69
EX67_ASPBR
ID   EX67_ASPBR     STANDARD;      PRT;   464 AA.
AC   P48766;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-FEB-1998 (Rel. 36, Last sequence update)
DT   15-OCT-2001 (Rel. 39, Last annotation update)
DE   Phosphomannomutase (EC 5.4.2.8) (PMM).
GN   EX67.
OS   Azospirillum brasilense.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
OC   Azospirillum.
OX   NCBI_TaxID=192;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN Sp7;
RA   Petersen D.J., Vanderleyden J.;
RL   Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: D-mannose 1-phosphate = D-mannose 6-phosphate.
CC   -!- SIMILARITY: BELONGS TO THE EUKARYOTIC PMM FAMILY.
CC   ---------- ----------------------------------------- ---------- ---
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CC
DR   EMBL; U23563; AAA69098.1; -.
DR   InterPro; IPR001347; PGM/PMM_mutase.
DR   Pfam; PF02878; PGM_PMM; 1.
DR   Pfam; PF02879; PGM_PMM_I; 1.
DR   Pfam; PF02880; PGM_PMM_II; 1.
DR   Pfam; PF02881; PGM_PMM_III; 1.
DR   PRINTS; PR00509; PGMPMM.
DR   PROSITE; PS00710; PGM_PMM; 1.
KW   Isomerase; Phosphorylation.
FT   ACT_SITE    106    106       FORMS THE PHOSPHOSERINE INTERMEDIATE
FT                                (BY SIMILARITY).
SQ   SEQUENCE   464 AA;  51130 MW;  82A7D1024E0FEE7C CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 464;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      207 KIESKELP 214
            ||||||||
Db      %% KIESKELP 41


RESULT 70
VNUC_IAB67
ID   VNUC_IAB67     STANDARD;      PRT;   464 AA.
AC   P17052;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Nucleoprotein.
GN   NP.
OS   Influenza A virus (strain A/Bel gium/33/89).
OS   Influenza A virus (strain A/Beijing/32/92).
OS   Influenza A virus (strain A/Beijing/353/89).
OS   Influenza A virus (strain A/Bucharest/6/89).
OS   Influenza A virus (strain A/Fukuoka/C/89).
OS   Influenza A virus (strain A/Memphis/14/85).
OS   Influenza A virus (strain A/Memphis/8/88), and
OS   Influenza A virus (strain A/Shandong/12/89).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenza A viruses; Influenzavirus A.
OX   NCBI_TaxID=8054, 8055, 7243, 8071, 8052, 8058, 11141, 8059;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93233249; PubMed=8517121;
RA   Shu L.L., Bean W.J., Webster R.G.;
RT   "Analysis of the evolution and variation of the human influenza A
RT   virus nucleoprotein gene from 1933 to 1990.";
RL   J. Virol. 67:2672-2729(1993).
CC   -!- FUNCTION: N. ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
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CC
DR   EMBL; L07374; AAA91486.1; -.
DR   EMBL; L07375; AAA91487.1; -.
DR   EMBL; L07376; AAA91488.1; -.
DR   EMBL; L07394; AAA91511.1; -.
DR   EMBL; L07377; AAA91494.1; -.
DR   EMBL; L07372; AAA91516.1; -.
DR   EMBL; L07373; AAA91483.1; -.
DR   EMBL; L07374; AAA91484.1; -.
DR   InterPro; IPR002141; Flu_NP.
DR   Pfam; PF00506; Flu_NP; 1.
KW   Nucleoprotein.
SQ   SEQUENCE   498 AA;  56224 MW;  23F5A7A7D8BC1BAF4 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 498;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      121 GPAVSSG 127
            |||||||
Db      282 GPAVSSG 288


RESULT 71
VNUC_IAH92
ID   VNUC_IAH92     STANDARD;      PRT;   498 AA.
AC   P19932;
DT   01-APR-1990 (Rel. 15, Created)
DT   01-APR-1990 (Rel. 15, Last sequence update)
DT   01-MAY-1992 (Rel. 22, Last annotation update)
DE   Nucleoprotein.
GN   NP.
OS   Influenza A virus (strain A/Port Rico/8/34).
```

OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11431;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE [illegible]; PubMed [illegible];
RA Gammelin M., Mandler J., Scholtissek C.;
RT "Two subtypes of nucleoproteins (NP) of influenza A [illegible]";
RL Virology 170:7[illegible]-80(1989).
CC -!- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
CC --
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CC --
DR EMBL; M22577; AAA43[illegible]1.1; -.
DR PIR; [illegible]; VHIVN[illegible].
DR PIR; [illegible]; [illegible].
DR InterPro; IPR002141; Flu_NP.
DR Pfam; PF00506; Flu_NP; 1.
KW Nucleoprotein.
SQ SEQUENCE 498 AA; 5[illegible] MW; [illegible] CRC64;

Query Match 2.1%; Score 7; DB 1; Length 498;
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches 7; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy 121 GPAVSSG 127
|||||||
Db 282 GPAVSSG 288

RESULT 11
VNUC_IAKI[illegible]
ID VNUC_IAKI[illegible] STANDARD; PRT; 498 AA.
AC [illegible];
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Nucleoprotein.
GN NP.
OS Influenza A virus (strain A/Kitakyushu/[illegible]/93).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=[illegible]2478;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 984[illegible]; PubMed 973[illegible];
RA Lindstrom S.E., Hiromoto Y., Nerome R., [illegible] K., [illegible],
RA Yamazaki Y., Takahashi T., Nerome K.;
RT "Phylogenetic analysis of the entire genome of influenza A (H3N2)
RT viruses from Japan: evidence for genetic reassortment of the six
RT internal genes.";
RL J. Virol. 72:[illegible](1998).
CC -!- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
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CC --
DR EMBL; AF[illegible]; AA[illegible]462.1; -.
DR InterPro; IPR002141; Flu_NP.
DR Pfam; PF00506; Flu_NP; 1.
KW Nucleoprotein.
SQ SEQUENCE 498 AA; 56[illegible] MW; [illegible] CRC64;

Query Match 2.1%; Score 7; DB 1; Length 498;
Best Local Similarity [illegible]; Pred. No. 52;
Matches 7; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps 0;

Qy 121 GPAVSSG 127
|||||||
Db 282 GPAVSSG 288

RESULT 12
VNUC_IAME[illegible]
ID VNUC_IAME[illegible] STANDARD; PRT; 498 AA.
AC Q07[illegible];
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Nucleoprotein.
GN NP.
OS Influenza A virus (strain A/Memphis/3/88).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38972;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE [illegible]; PubMed [illegible];
RA Shu L.L., Bean W.J., Webster R.G.;
RT "Analysis of the evolution and variation of the human influenza A
RT virus nucleoprotein gene from 1933 to 1990.";
RL J. Virol. 67:2723-2729(1993).
CC -!- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
CC --
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CC --
DR EMBL; L07369; AAA514[illegible]; -.
DR InterPro; IPR002141; Flu_NP.
DR Pfam; PF00506; Flu_NP; 1.
KW Nucleoprotein.
SQ SEQUENCE 498 AA; 56[illegible] MW; [illegible] CRC64;

Query Match 2.1%; Score 7; DB 1; Length 498;
Best Local Similarity [illegible]; Pred. No. 52;
Matches 7; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy 121 GPAVSSG 127
|||||||
Db 282 GPAVSSG 288

RESULT 13
VNUC_IAME[illegible]
ID VNUC_IAME[illegible] STANDARD; PRT; 498 AA.
AC Q07548;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Nucleoprotein.
GN NP.
OS Influenza A virus (strain A/Memphis/[illegible]/80).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38975;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE [illegible]; PubMed 84[illegible];
RA Shu L.L., Bean W.J., Webster R.G.;
RT "Analysis of the evolution and variation of the human influenza A

```
RT   virus nucleoprotein gene from 1933 to 1995.";
RL   J. Virol. 67:2723-2729(1993).
CC    ! FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
CC
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CC
DR   EMBL; L07266; AAA43512.1; -.
DR   InterPro; IPR000234; Flu_NP.
DR   Pfam; PF00506; Flu_NP; 1.
KW   Nucleoprotein.
SQ   SEQUENCE   498 AA;  56296 MW;  6CB52A8122A4F0A7 CRC64;

  Query Match              2.1%;  Score 7;  DB 1;  Length 498;
  Best Local Similarity   50.0%;  Pred. No. 5.2;
  Matches    7;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy     121 GAAVSGT 127
           ||||||| |||
Db     282 GAAVSGT 288


RESULT 11
VNP0_IAMEP
ID   VNP0_IAMEP     STANDARD;      PRT;   498 AA.
AC   Q07543;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Nucleoprotein.
GN   NP.
OS   Influenza A virus (strain A/Memphis/4/89).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenza A viruses; Influenzavirus A.
OX   NCBI_TaxID=11344;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93233239; PubMed=8474171;
RA   Shu L.L., Bean W.J., Webster R.G.;
RT   "Analysis of the evolution and variation of the human influenza A
RT   virus nucleoprotein gene from 1933 to 1990.";
RL   J. Virol. 67:2723-2729(1993).
CC    ! FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
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CC
DR   EMBL; L07266; AAA43512.1; -.
DR   InterPro; IPR000234; Flu_NP.
DR   Pfam; PF00506; Flu_NP; 1.
KW   Nucleoprotein.
SQ   SEQUENCE   498 AA;  56296 MW;  6CB52A8122A4F0A7 CRC64;

  Query Match              2.1%;  Score 7;  DB 1;  Length 498;
  Best Local Similarity   50.0%;  Pred. No. 5.2;
  Matches    7;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy     121 GAAVSGT 127
           ||||||| |||
Db     282 GAAVSGT 288


RESULT 12
VNP0_IAMEP
ID   VNP0_IAMEP     STANDARD;      PRT;   498 AA.
AC   Q07542;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Nucleoprotein.
GN   NP.
OS   Influenza A virus (strain A/Shandong/9/93).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenza A viruses; Influenzavirus A.
OX   NCBI_TaxID=38985;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93233239; PubMed=8474171;
RA   Shu L.L., Bean W.J., Webster R.G.;
RT   "Analysis of the evolution and variation of the human influenza A
RT   virus nucleoprotein gene from 1933 to 1990.";
RL   J. Virol. 67:2723-2729(1993).
CC    ! FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
CC
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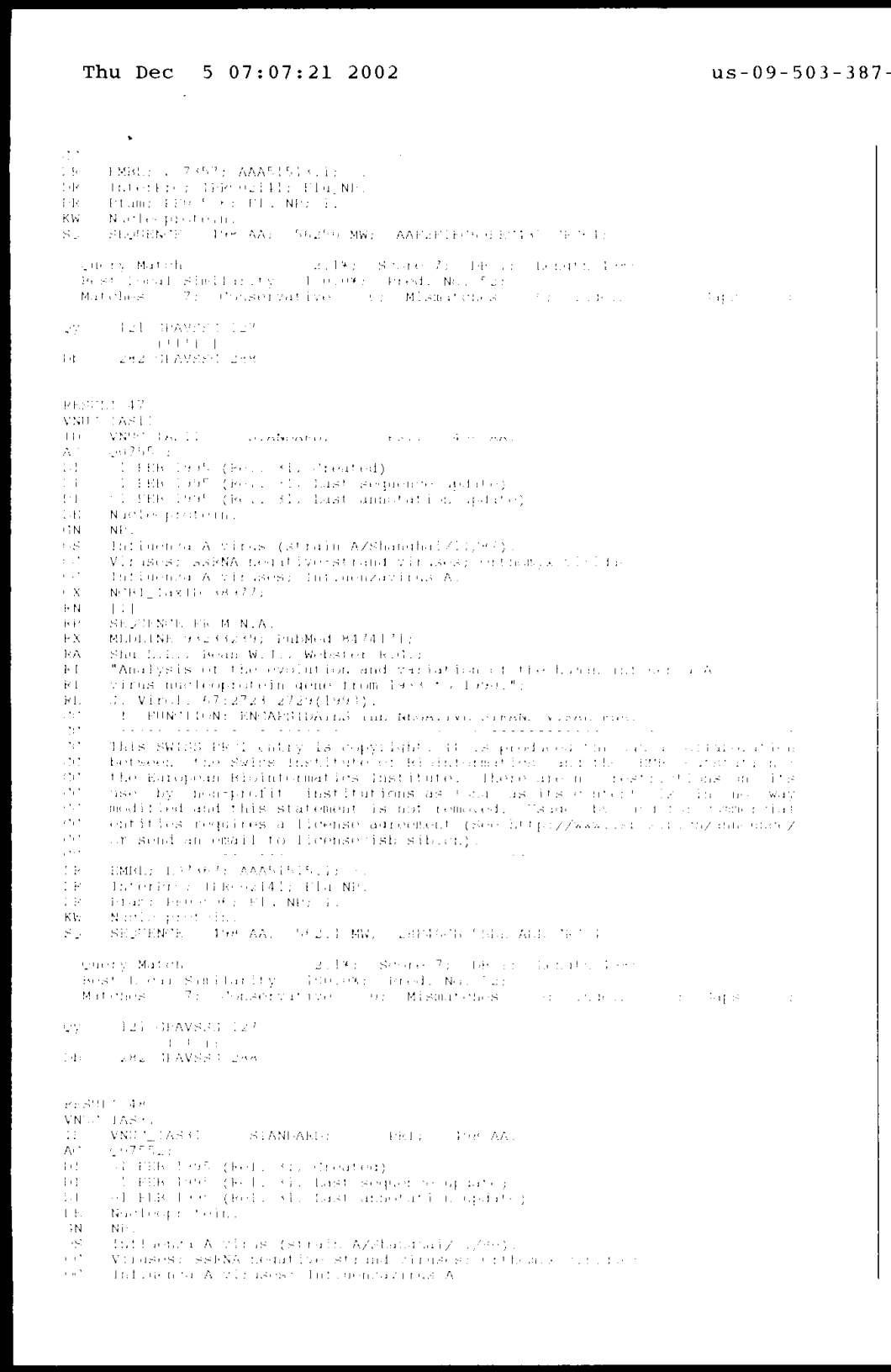

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QY      1: GPAVSSV 7
           |||||||
Db      29: GPAVSSV 35


RESULT 56
IXK_HUMAN
ID   IXK_HUMAN       STANDARD;       PRT;   [illegible] AA.
AC   P42680; Q15226;
DT   01-NOV-1995 (rel. 32, Created)
DT   01-FEB-1996 (rel. 33, Last sequence update)
DT   15-JUN-2002 (rel. 41, Last annotation update)
DE   Tyrosine protein kinase IXK (EC 2.7.1.112).
GN   IXK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96164775; PubMed=8601313;
RA   Bolen J.B., Rowley R.B., Spana C., Tsygankov A.Y.;
RT   "IXK, a novel human tyrosine kinase expressed in [illegible]
RT   sequence identity with the family kinases and maps to [illegible]";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:1732-1736(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96164775; PubMed=8601313;
RA   Rowley R.B., Burkhardt A.L., Chao H.G., Matsueda G.R., Bolen J.B.;
RA   Lillman G.W.;
RT   "Human IXK: genomic organization, structure and [illegible]
RT   [illegible] with the Ick gene.";
RL   Submitted (29-MAY-1995).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN T CELLS AND B MEMBRANE [illegible]
CC       LINES.
CC   -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC       SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC   ---------- [illegible] ----------
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CC   ----------
DR   EMBL; L27071; AAA74572.1; -.
DR   EMBL; U43479; AAB60412.1; -.
DR   EMBL; U43467; AAB60412.1; JOINED.
DR   EMBL; U43468; AAB60412.1; JOINED.
DR   EMBL; U43469; AAB60412.1; JOINED.
DR   EMBL; U43470; AAB60412.1; JOINED.
DR   EMBL; U43471; AAB60412.1; JOINED.
DR   EMBL; U43472; AAB60412.1; JOINED.
DR   EMBL; U43473; AAB60412.1; JOINED.
DR   EMBL; U43474; AAB60412.1; JOINED.
DR   EMBL; U43475; AAB60412.1; JOINED.
DR   EMBL; U43476; AAB60412.1; JOINED.
DR   EMBL; U43477; AAB60412.1; JOINED.
DR   EMBL; U43478; AAB60412.1; JOINED.
DR   HSSP; Q00587; 1AWX.
DR   GenAtlas; HGNC:1,3x4; IXK.
DR   MIM; 600,0[illegible];
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000[illegible] SH2.
DR   InterPro; IPR000452; SH3.
DR   InterPro; IPR000[illegible] tyr_pkinase.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   ProDom; PD000[illegible]; SH2; 1.
DR   ProDom; PD000[illegible]; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrK; 1.
DR   PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR   PROSITE; PS00108; PROTEIN KINASE TYR; 1.
DR   PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Transferase; Tyrosine protein kinase; ATP-binding; SH2 domain;
KW   SH3 domain; Phosphorylation.
FT   DOMAIN        14      74       POLY-CYS.
FT   DOMAIN        58      73       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   DOMAIN        82     174       SH2.
FT   DOMAIN       180     240       SH3.
FT   DOMAIN       271     527       PROTEIN KINASE.
FT   NP_BIND      277     285       ATP (BY SIMILARITY).
FT   BINDING      295     295       ATP (BY SIMILARITY).
FT   ACT_SITE     386     386       BY SIMILARITY.
FT   MOD_RES      420     420       PHOSPHORYLATION (AUTO ?) (BY SIMILARITY).
FT   CONFLICT      45      45       H -> R (IN REF. 2).
SQ   SEQUENCE   527 AA;  61239 MW;  D[illegible]E4C [illegible]

  Query Match             2.1%;  Score 7;  DB 1;  Length 527;
  Best Local Similarity   100.0%;  Pred. No. 55;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 PLPPLPP 11
          |||||||
Db     71 PLPPLPP 77


Search completed: December 5, 2002, 06:54:12
Job time : 19 secs
```

OM protein - protein search, using sw model

Run on: December 5, 2002, 06:57:12 ; Search time 0 seconds
(without alignments)
1905.711 Million cell updates/sec

Title: US-09-503-387-3

Perfect score: 539

Sequence: 1 MSFSFIAEFCSRVLGRVEA.....KSPSISGSP 539

Scoring table: GIX
Gapop 10.0 , Gapext 0.5

Searched: 67138 seqs, 20604112 residues

Word size: 4

Total number of hits satisfying chosen parameters: 67138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_rest:*
8: sp_unassigned:*
9: sp_plastid:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_otherclassified:*
15: sp_environmental:*
16: sp_bacteriophage:*
17: sp_archaeaphage:*

Prel. No.: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score histogram.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	539	100.0	539	4	Q9EIE2	Q9EIE2 Sapien
2	259	48.4	620	4	Q9BCN6	Q9BCN6 Sapien
3	203	37.9	823	4	Q9BCN7	Q9BCN7 Sapien
4	11	2.2	11	4	Q9BCN5	Q9BCN5 Sapien
5	11	2.2	299	4	Q25C18	Q25C18 Sapien
6	11	2.2	469	4	Q25C19	Q25C19 Sapien
7	10	1.9	151	4	Q9C0Z2	Q9C0Z2 Sapien
8	10	1.9	153	4	Q9C0A6	Q9C0A6 Sapien
9	10	1.9	173	4	Q9BN87	Q9BN87 Sapien
10	10	1.9	272	4	Q9BC90	Q9BC90 Sapien
11	9	1.7	262	4	Q9BS82	Q9BS82 Sapien
12	9	1.7	265	4	Q9BN07	Q9BN07 Sapien
13	9	1.7	268	4	Q9BN05	Q9BN05 Sapien
14	10	1.9	268	4	Q9BN04	Q9BN04 Sapien
15	9	1.7	283	4	Q9BNB9	Q9BNB9 Sapien
16	9	1.7	284	4	Q14495	Q14495 Sapien
17	9	1.7	284	4	Q9BN06	Q9BN06 Sapien
18	9	1.7	284	4	Q9C1L8	Q9C1L8 Sapien
19	9	1.7	287	4	Q9BS85	Q9BS85 Sapien
20	9	1.7	287	4	Q9BS84	Q9BS84 Sapien
21	10	1.9	288	4	Q9BN08	Q9BN08 Sapien
22	10	1.9	290	4	Q9BN31	Q9BN31 Sapien
23	9	1.7	293	4	Q9BN33	Q9BN33 Sapien
24	10	1.9	293	4	Q9BNB5	Q9BNB5 Sapien
25	10	1.9	293	4	Q9BN13	Q9BN13 Sapien
26	10	1.9	293	4	Q9BN17	Q9BN17 Sapien
27	10	1.9	293	4	Q9BNB6	Q9BNB6 Sapien
28	10	1.9	293	4	Q9BNB5	Q9BNB5 Sapien
29	10	1.9	293	4	Q9BM51	Q9BM51 Sapien
30	10	1.9	304	4	Q14754	Q14754 Sapien
31	10	1.9	304	2	Q9BDR0	Q9BDR0 Sapien
32	10	1.9	311	4	Q9C1J9	Q9C1J9 Sapien
33	10	1.9	330	4	Q9BSJ2	Q9BSJ2 Homo s
34	10	1.9	411	4	Q14444	Q14444 Sapien
35	10	1.9	441	4	Q14447	Q14447 Sapien
36	10	1.9	441	4	P84092	P84092 Homo s
37	10	1.9	444	4	Q14446	Q14446 Sapien
38	10	1.9	444	4	Q14447	Q14447 Sapien
39	10	1.9	445	4	P78504	P78504 Homo s
40	10	1.9	473	4	Q9C5Z6	Q9C5Z6 Sapien
41	10	1.9	475	4	Q9BDI4	Q9BDI4 Sapien
42	10	1.9	475	4	P84090	P84090 Homo s
43	10	1.9	475	4	P82970	P82970 Homo s
44	10	1.9	484	4	Q9BE63	Q9BE63 Sapien
45	10	1.9	484	7	Q9C4A6	Q9C4A6 Sapien
46	10	1.9	484	4	Q15466	Q15466 Sapien
47	10	1.9	484	4	Q9C4J6	Q9C4J6 Sapien
48	10	1.9	484	4	Q9BEB2	Q9BEB2 Sapien
49	10	1.9	484	4	Q9BEB1	Q9BEB1 Sapien
50	10	1.9	484	4	Q9BEB3	Q9BEB3 Sapien
51	10	1.9	484	5	Q9BD09	Q9BD09 Sapien
52	10	1.9	486	6	Q95L81	Q95L81 Macaca
53	10	1.9	487	4	Q96JH6	Q96JH6 Sapien
54	10	1.9	487	7	Q96A67	Q96A67 Sapien
55	10	1.9	488	7	Q96A68	Q96A68 Sapien
56	10	1.9	490	4	Q15320	Q15320 Sapien
57	10	1.9	668	11	Q5R0C2	Q5R0C2 Pan tro
58	10	1.9	681	4	Q9BQ24	Q9BQ24 Homo s
59	10	1.9	682	4	Q9BQ26	Q9BQ26 Sapien
60	10	1.9	690	11	Q9D434	Q9D434 Mus mus
61	10	1.9	690	11	Q9R001	Q9R001 Mus musc
62	9	1.7	488	4	Q9BJD2	Q9BJD2 Homo s
63	9	1.7	512	4	Q9BMA1	Q9BMA1 Homo s
64	9	1.7	4??	2	Q9BW39	Q9BW39 Selaco
65	9	1.7	5??	10	Q9DCV4	Q9DCV4 Gallus
66	9	1.7	5??	11	Q9DFX5	Q9DFX5 Mus mus
67	9	1.7	5??	16	Q9VKN7	Q9VKN7 Drosoph
68	9	1.7	6??	5	Q9BW50	Q9BW50 Odontog
69	9	1.7	7??	2	Q9XUH2	Q9XUH2 Hyoxal
70	9	1.7	8??	5	Q27233	Q27233 Spodopt
71	9	1.7	1??	11	Q8R458	Q8R458 Mus mus
72	9	1.7	1??	11	Q8R457	Q8R457 Mus mus
73	8	1.4	134	11	Q9D840	Q9D840 Mus musc
74	8	1.4	2??	15	Q9QEP6	Q9QEP6 Spodop
75	8	1.4	1??	4	Q9N1C8	Q9N1C8 Sapien

ALIGNMENTS

RESULT 1
Q9EIE2
ID Q9EIE2 PRELIMINARY; PRT; 539 AA.
AC Q9EIE2;
DT 01-MAY-2001 (TREMBLrel. 14, Created)
DT 01-MAY-2001 (TREMBLrel. 14, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 15, Last annotation update)
DE Platelet glycoprotein V precursor (Platelet glycoprotein V) (
GN GPV.

OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Miura Y.;
RT "Platelet glycoprotein VI.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=11827954;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI.";
RL Biochem. Biophys. Res. Commun. 277:27-36(2000).
DR EMBL; AB053273; BAA89954.1; -.
DR EMBL; AB061021; BAB12247.1; -.
DR HSSP; P43626; 1NKK.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_tyr.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv2; 2.
DR SMART; SM00410; IG_like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 320 AA; 37008 MW; FERE4A7FFE7D15C9C4;

Query Match 70.4%; Score 250; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.8e-20;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPSPLALFCLGLCLGPVPAQSGLLDKESVALSSLVPLPKPVLLRQEDVLGYKLF 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MSPSPLALFCLGLCLGPVPAQSGLLDKESVALSSLVPLPKPVLLRQEDVLGYKLF 60

Qy 61 KLSSDSFYQKQAVLPPAMKSSRAGFYLAYYSLGSSAKKSPTFTLTIYKGTRVFE 240
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 KLSSDSFYQKQAVLPPAMKSSRAGFYLAYYSLGSSAKKSPTFTLTIYKGTRVFE 240

Qy 241 TESPSFLLSPKESDSFAGFALYPAENQVPADPGVTKEDREDCLTLSLKGNTVFE 400
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TESPSFLLSPKESDSFAGFALYPAENQVPADPGVTKEDREDCLTLSLKGNTVFE 400

Qy 401 EGFAVSRSVQMSFRVGSLGFPMSSKSHFMSEVSVNVSQMPSSGKSTKLFEVHLR 560
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 401 EGFAVSRSVQMSFRVGSLGFPMSSKSHFMSEVSVNVSQMPSSGKSTKLFEVHLR 560

Qy 561 PVGMAEELIENSVDAVAATSVAVMVTEDDSEPSEGDTVLSGYGADHSGNTSDEL 720
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 561 PVGMAEELIENSVDAVAATSVAVMVTEDDSEPSEGDTVLSGYGADHSGNTSDEL 720

Qy 721 ETSMLKSSHSWVFSKDASFLHWLEVPEEDKEGAEFDDVSLYHDPIKVTGVVRQL 880
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 ETSMLKSSHSWVFSKDASFLHWLEVPEEDKEGAEFDDVSLYHDPIKVTGVVRQL 880

Qy 881 KLASVEMKLETLRSCTQQMACTLGIAGKVADMSASMEKRLNQESSRASSVMKL 1040
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 881 KLASVEMKLETLRSCTQQMACTLGIAGKVADMSASMEKRLNQESSRASSVMKL 1040

Qy 1041 LKMSLEIGSNVQDRHLSGAATGTPTNVTTKASKMVETIDMDDIQTFAKDNEMA 1200
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1041 LKMSLEIGSNVQDRHLSGAATGTPTNVTTKASKMVETIDMDDIQTFAKDNEMA 1200

Qy 1201 EDDPKDRFEKRKNQLLLAICDKVFRWMKFVAEEMNVILGNKPEHLVKDCLQEH 1360
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 EDDPKDRFEKRKNQLLLAICDKVFRWMKFVAEEMNVILGNKPEHLVKDCLQEH 1360

Qy 1361 QEISSASHVMKRMIADTEGSILAYRSKDHLWNSDTGKNGIYHVAVQSTGSIIE 1520
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1361 QEISSASHVMKRMIADTEGSILAYRSKDHLWNSDTGKNGIYHVAVQSTGSIIE 1520

Qy 1521 TESPSFLLSPKESDSFAGFALYPAENQVPADPGVTKEDREDCLTLSLKGNTVFE 1680
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1521 TESPSFLLSPKESDSFAGFALYPAENQVPADPGVTKEDREDCLTLSLKGNTVFE 1680

Qy 1681 EGFAVSRSVQMSFRVGSLGFPMSSKSHFMSEVSVNVSQMPSSGKSTKLFEVHLR 1840
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1681 EGFAVSRSVQMSFRVGSLGFPMSSKSHFMSEVSVNVSQMPSSGKSTKLFEVHLR 1840

Qy 1841 PVGMAEELIENSVDAVAATSVAVMVTEDDSEPSEGDTVLSGYGADHSGNTSDEL 2000
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1841 PVGMAEELIENSVDAVAATSVAVMVTEDDSEPSEGDTVLSGYGADHSGNTSDEL 2000

Qy 2001 ETSMLKSSHSWVFSKDASFLHWLEVPEEDKEGAEFDDVSLYHDPIKVTGVVRQL 2160
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2001 ETSMLKSSHSWVFSKDASFLHWLEVPEEDKEGAEFDDVSLYHDPIKVTGVVRQL 2160

Qy 2161 KLASVEMKLETLRSCTQQMACTLGIAGKVADMSASMEKRLNQESSRASSVMKL 2320
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2161 KLASVEMKLETLRSCTQQMACTLGIAGKVADMSASMEKRLNQESSRASSVMKL 2320

RESULT 3
Q9HBN7
ID Q9HBN7 PRELIMINARY; PRT; 320 AA.
AC Q9HBN7;
DT 01-MAR-2001 (TrEMBLrel. 15, Created)
DT 01-MAR-2001 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 16, Last annotation update)
DE Platelet glycoprotein VI 2.
GN GPVI.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20418073; PubMed=11027934;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI.";
RT Biochem. Biophys. Res. Commun. 277:27-36(2000).
DR EMBL; AB053273; BAB12247.1; -.
DR HSSP; P43626; 1NKK.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_tyr.
DR InterPro; IPR003006; Ig_like.
DR InterPro; IPR003006; Ig_MHC.

ID Plus; PRT; [illegible] AA.
XX SMART; SM00040; [illegible]
XX SMART; SM00409; [illegible]
KW Immunoglobulin domain.
SQ SEQUENCE [illegible] AA; [illegible] MW; [illegible]

Query Match [illegible]; Score [illegible]; DB 4; Length [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

RESULT 4
[illegible]
ID [illegible] PRELIMINARY; PRT; [illegible] AA.
AC [illegible];
DT [illegible] (first entry)
DT [illegible] (last sequence update)
DT [illegible] (last annotation update)
DE [illegible]
GN [illegible]
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=[illegible];
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; [illegible]; PubMed [illegible];
RA [illegible];
RT "[illegible]";
RL [illegible].
DR EMBL; [illegible]; [illegible].
DR HSSP; [illegible]; 1NKR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGc1; 1.
SQ SEQUENCE [illegible] AA; [illegible] MW; [illegible]

Query Match [illegible]; Score [illegible]; DB 4; Length [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

Qy [illegible]
Db [illegible]

RESULT 5
[illegible]
ID [illegible] PRELIMINARY; PRT; [illegible] AA.
AC [illegible];
DT [illegible] (first entry)
DT [illegible] (last sequence update)
DT [illegible] (last annotation update)
DE [illegible]
GN [illegible]
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=[illegible];
RN [1]
RP SEQUENCE FROM N.A.
RA [illegible];
RT "[illegible]";
RL [illegible].
DR EMBL; [illegible]; [illegible].
DR HSSP; [illegible]; 1NKR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGc1; 1.
SQ SEQUENCE [illegible] AA; [illegible] MW; [illegible]

Query Match [illegible]; Score [illegible]; DB 4; Length [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

Qy [illegible]
Db [illegible]

RESULT 6
[illegible]
ID [illegible] PRELIMINARY; PRT; [illegible] AA.
AC [illegible];
DT [illegible] (first entry)
DT [illegible] (last sequence update)
DT [illegible] (last annotation update)
DE [illegible]
GN [illegible]
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=[illegible];
RN [1]
RP SEQUENCE FROM N.A.
RA [illegible];
RT "[illegible]";
RL [illegible].
DR EMBL; [illegible]; [illegible].
DR HSSP; [illegible]; 1NKR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGc1; 1.
SQ SEQUENCE [illegible] AA; [illegible] MW; [illegible]

Query Match [illegible]; Score [illegible]; DB 4; Length [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

Qy [illegible]
Db [illegible]

RESULT 7
[illegible]
ID [illegible] PRELIMINARY; PRT; [illegible] AA.
AC [illegible];
DT [illegible] (first entry)
DT [illegible] (last sequence update)
DT [illegible] (last annotation update)
DE Putative inhibitory receptor (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```
RX   MEDLINE; 97161664; PubMed; 9077169;
RA   Rojo S., Borrego F., Lopez-Botet M., Coligan J.E.;
RT   "Type I transmembrane receptor with inhibitory function in T lymphocytes and NK cells.";
RL   J. Immunol. 158:5 (1997).
DR   EMBL; U75666; AAC50628.1;
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR001652; 1a.
DR   InterPro; IPR003599; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
FT   NON_TER       151     151
SQ   SEQUENCE   151 AA;  16464 MW;  CE6D9A4D2F6C2CB3 CRC64;

  Query Match             2.0%;  Score 12;  DB 4;  Length 151;
  Best Local Similarity   100.0%;  Pred. No. 0.0056;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SGPELVVKP 9
          ||||||||| |
Db     143 SGPELVVKP 151


RESULT 8
Q6DJA2
ID   Q6DJA2_      PRELIMINARY;      PRT;   166 AA.
AC   Q6DJA2;
DT   31-MAY-2006 (TrEMBLrel. 34, Created)
DT   31-MAY-2006 (TrEMBLrel. 34, Last sequence update)
DT   31-OCT-2006 (TrEMBLrel. 39, Last annotation update)
DE   NK receptor (Fragment).
GN   KIR 3DL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chan H.W., Sadikmamilla K., Salter R.D.;
RT   "NK receptors with divergent cytoplasmic domains are encoded by genes
RT   with similar exon structures.";
RL   Submitted (MAY-2006) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF513661; AAM94796.1;  -.
DR   EMBL; AF513662; AAM94797.1; JOINED.
DR   EMBL; AF513663; AAM94798.1; JOINED.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
FT   NON_TER       1       1
SQ   SEQUENCE   166 AA;  18104 MW;  22A6630A43B71EEC CRC64;

  Query Match             2.0%;  Score 12;  DB 4;  Length 166;
  Best Local Similarity   100.0%;  Pred. No. 0.0062;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SGPELVVKP 9
          ||||||||| |
Db     158 SGPELVVKP 166


RESULT 9
Q9GNC7
ID   Q9GNC7      PRELIMINARY;      PRT;   120 AA.
AC   Q9GNC7;
DT   01-MAY-2000 (TrEMBLrel. 14, Created)
DT   01-MAY-2000 (TrEMBLrel. 14, Last sequence update)
DT   31-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   P58 killer cell activating receptor KAR KIR (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99451717; PubMed=10424161;
RA   Chewae Y.J., Cho S.E., Kim S.C., Kim T.;
RT   "Diversity of the repertoire of p58 killer cell inhibitory receptors
RT   in a single individual.";
RL   Immunol. Lett. 66:267-274(1999).
DR   EMBL; AF135064; AAD46458.1;  -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR001652; 1a.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
FT   NON_TER       1       1
SQ   SEQUENCE   120 AA;  13784 MW;  1174A9AE3171EEA CRC64;

  Query Match             2.0%;  Score 12;  DB 4;  Length 120;
  Best Local Similarity   100.0%;  Pred. No. 0.0064;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SGPELVVKP 9
          ||||||||| |
Db     112 SGPELVVKP 120


RESULT 10
Q9GNC8
ID   Q9GNC8      PRELIMINARY;      PRT;   202 AA.
AC   Q9GNC8;
DT   01-MAY-2000 (TrEMBLrel. 14, Created)
DT   01-MAY-2000 (TrEMBLrel. 14, Last sequence update)
DT   31-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   P58 killer cell activating receptor KAR KIR (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99451717; PubMed=10424161;
RA   Chewae Y.J., Cho S.E., Kim S.C., Kim T.;
RT   "Diversity of the repertoire of p58 killer cell inhibitory receptors
RT   in a single individual.";
RL   Immunol. Lett. 66:267-274(1999).
DR   EMBL; U96288; AAB54128.1;  -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR001652; 1a.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
FT   NON_TER       1       1
SQ   SEQUENCE   202 AA;  22284 MW;  0F3E7A6A0E477EB0 CRC64;

  Query Match             2.0%;  Score 12;  DB 4;  Length 202;
  Best Local Similarity   100.0%;  Pred. No. 0.0076;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SGPELVVKP 9
          ||||||||| |
Db     107 SGPELVVKP 115


RESULT 11
Q9GNB2
ID   Q9GNB2      PRELIMINARY;      PRT;   154 AA.
AC   Q9GNB2;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
```

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ID   ...
AC   ...
DT   ... (TrEMBLrel. ..., Last annotation update)
DE   P58 NK cell inhibitory receptor KIR KF (Fragment).
GN   KIR KF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; ...
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; ...
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99451217; PubMed=10424443;
RA   Chwae Y.J., Cho S.E., Kim S.J., Kim J.;
RT   "Diversity of the repertoire of p58 Killer cell inhibitory receptors
RT   in a single individual.";
RL   Immunol. Lett. 68:267-274(1999).
DR   EMBL; AF...; AAD...; -.
DR   BSSP; P43626; INKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
FT   NON_TER       1       1
SQ   SEQUENCE   203 AA;  22102 MW;  ...

  Query Match             ...%;  Score ...;  DB 4;  Length ...
  Best Local Similarity   ...%;  Pred. No. ...;
  Matches  ...;  Conservative  ...;  Mismatches  ...;  Indels  ...;  Gaps  ...;

Qy      ... KPSLSAQPGP 122
                ||
Db      ... KPSLSAQPGP 116


RESULT 12
Q...
ID   Q...       PRELIMINARY;      PRT:   203 AA.
AC   Q...;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   P58 killer cell inhibitory receptor KIR KF (Fragment)
GN   KIR KF.
OS   Homo Sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; ...
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; ...
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99451217; PubMed=10424443;
RA   Chwae Y.J., Cho S.E., Kim S.J., Kim J.;
RT   "Diversity of the repertoire of p58 killer cell inhibitory receptors
RT   in a single individual.";
RL   Immunol. Lett. 68:267-274(1999).
DR   EMBL; AF...; AAD...; -.
DR   BSSP; P43626; INKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
FT   NON_TER       1       1
FT   NON_TER     203     203
SQ   SEQUENCE   203 AA;  22...  MW;  ...

  Query Match             ...%;  Score ...;  DB 4;  Length ...
  Best Local Similarity   ...%;  Pred. No. ...;
  Matches  ...;  Conservative  ...;  Mismatches  ...;  Indels  ...;  Gaps  ...;

Qy      ... KPSLSAQPGP 122
                ||||||||||
Db      ... KPSLSAQPGP 116


RESULT 13
Q...
ID   Q...       PRELIMINARY;      PRT:   203 AA.
AC   Q...;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   P58 killer cell inhibitory receptor KIR KF (Fragment)
GN   KIR KF.
OS   Homo Sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; ...
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; ...
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99451217; PubMed=10424443;
RA   Chwae Y.J., Cho S.E., Kim S.J., Kim J.;
RT   "Diversity of the repertoire of p58 killer cell inhibitory receptors
RT   in a single individual.";
RL   Immunol. Lett. 68:267-274(1999).
DR   EMBL; AF...; AAD...; -.
DR   BSSP; P43626; INKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
FT   NON_TER       1       1
FT   NON_TER     203     203
SQ   SEQUENCE   203 AA;  22...  MW;  ...

  Query Match             ...%;  Score ...;  DB 4;  Length ...
  Best Local Similarity   ...%;  Pred. No. ...;
  Matches  ...;  Conservative  ...;  Mismatches  ...;  Indels  ...;  Gaps  ...;

Qy      ... KPSLSAQPGP 122
                ||||||||||
Db      ... KPSLSAQPGP 116


RESULT 14
Q...
ID   Q...       PRELIMINARY;      PRT:   203 AA.
AC   Q...;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   P58 killer cell inhibitory receptor KIR KF (Fragment)
GN   KIR KF.
OS   Homo Sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; ...
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; ...
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99451217; PubMed=10424443;
RA   Chwae Y.J., Cho S.E., Kim S.J., Kim J.;
RT   "Diversity of the repertoire of p58 killer cell inhibitory receptors
RT   in a single individual.";
RL   Immunol. Lett. 68:267-274(1999).
DR   EMBL; AF...; AAD...; -.
DR   BSSP; P43626; INKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
FT   NON_TER       1       1
FT   NON_TER     203     203
SQ   SEQUENCE   203 AA;  22...  MW;  ...

  Query Match             ...%;  Score ...;  DB 4;  Length ...
```

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  Best Local Similarity   100.0%;  Pred. No. 0.0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LLVKPSKLSAQDQP 122
          ||||||||||||||
Db      1 LLVKPSKLSAQDQP 114


RESULT 15
Q9UNK0
ID   Q9UNK0      PRELIMINARY;      PRT;   205 AA.
AC   Q9UNK0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   P58 killer cell inhibitory receptor KIR KIR (Fragment).
GN   KIR KIR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20552717; PubMed=10942414;
RA   Chewa Y.G., Cho S.G., Kim S.Y., Kim T.;
RT   "Diversity of the repertoire of p58 killer cell inhibitory receptor
RT   in a single individual.";
RL   Immunol. Lett. 74:262-274(2000).
DR   EMBL; AF154562; AAD24479.1; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR001650; Lg.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
FT   NON_TER     1     1
FT   NON_TER   203   203
SQ   SEQUENCE   203 AA;  22256 MW;  C1FFF9C1F6BC79AF CRC64;

  Query Match             2.9%;  Score 10;  DB 4;  Length 203;
  Best Local Similarity   1.1%;  Pred. No. 2.7;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LLVKPSKLSAQDQP 122
          ||||||||||||||
Db     10 LLVKPSKLSAQDQP 123


RESULT 16
Q9UNK1
ID   Q9UNK1      PRELIMINARY;      PRT;   204 AA.
AC   Q9UNK1;
DT   01-NOV-2000 (TrEMBLrel. 01, Created)
DT   01-NOV-2000 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Nkat7 delta 2a1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20552717; PubMed=10942414;
RA   Uehrvec P., Samaridis J., Cerianna M.;
RT   "Alternatively spliced forms of human killer inhibitory receptors.";
RL   Immunogenetics 51:227-238(2000).
DR   EMBL; AF154563; AAD24480.1; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR001650; Lg.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
SQ   SEQUENCE   204 AA;  22411 MW;  [illegible] CRC64;

  Query Match             2.9%;  Score 10;  DB 4;  Length 204;
  Best Local Similarity   1.1%;  Pred. No. 2.7;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LLVKPSKLSAQDQP 122
          ||||||||||||||
Db     11 LLVKPSKLSAQDQP 124


RESULT 17
Q95JL7
ID   Q95JL7      PRELIMINARY;      PRT;   221 AA.
AC   Q95JL7;
DT   01-MAY-2003 (TrEMBLrel. 13, Created)
DT   01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2003 (TrEMBLrel. 19, Last annotation update)
DE   Killer inhibitory receptor 3.1.2 (Fragment).
GN   KIR3L2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Chae I., Kim Y.M., Ahn J.M., Kim S.S., Kim J., Kim S.H., Park S.B.;
RT   "Genomic organization of novel genes encoding human killer inhibitory
RT   receptors.";
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF154315; AAD24479.1; -.
DR   EMBL; AF154312; AAD24479.1; JOINED.
DR   EMBL; AF154313; AAD24479.1; JOINED.
DR   EMBL; AF154315; AAD24479.1; JOINED.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR001650; Lg.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
FT   NON_TER     221     221
SQ   SEQUENCE   221 AA;  24243 MW;  C1CEFAAE3C64FA84 CRC64;

  Query Match             2.9%;  Score 10;  DB 4;  Length 221;
  Best Local Similarity   1.1%;  Pred. No. 2.7;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LLVKPSKLSAQDQP 122
          ||||||||||||||
Db     28 LLVKPSKLSAQDQP 137


RESULT 18
Q9BPE8
ID   Q9BPE8      PRELIMINARY;      PRT;   223 AA.
AC   Q9BPE8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Natural killer associated transcript 2 (Fragment).
GN   KIR2DL4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Samaridis J., Colonna M.;
RT   "Cloning of novel immunoglobulin superfamily receptors expressed on
RT   human myeloid and lymphoid cells: structural evidence for new stimulatory
RA   Borkhardt Schultz K., Bilbao L., Jones D., Fawcett M., Sillibourne S.,
RA   Pahl H., Vellaso N., De L., Pekrun W., Terry A., Santos I.,
RA   Jansmann L., Eder A., Christensen M., Gerdemann A., Azzoni L., Lo S.,
RA   Alitalo K., Andreesen R., Lunkenheim M., Ambros Keller T., Costello L.,
RA   Duarte S., Lopes S., Bruges R., Thomas P., Quan G., Krumlieder B.,
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RA   Arcangeli A., Sanders T., de Jo., Nelson M., Brandt S., Bianchi A.
RA   Jones A.G., Ferreira A.V.,
RT   "Sequence analysis of a 288 kb region in Tetraodon nigroviridis
RT   cloned in YACs.";
RL   Submitted (JAN 1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ392144; AAK96106.1; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
FT   NON_TER     279    279
SQ   SEQUENCE   279 AA;  29115 MW;  9A5A6A2A84A8E4CE CRC64;

  Query Match          27.9%;  Score 105;  DB 1;  Length 279;
  Best Local Similarity   100.0%;  Pred. No. 0.0009;
  Matches  105;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      113 KPSLSAQPGP 122
            ||||||||||
Db      128 KPSLSAQPGP 137


RESULT 19
AJ392144
ID   AJ392144       PRELIMINARY;      PRT;   279 AA.
AC   AJ392144;
DT   01-JUN-1999 (TREMBLrel. 06, Created)
DT   01-JUN-1999 (TREMBLrel. 06, Last sequence update)
DT   01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE   NK receptor precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [...]
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PERIPHERAL;
RA   Biassoni R.;
RL   Submitted (OCT 1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ002165; CAA05184.1; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
KW   Receptor; Signal.
FT   SIGNAL       1      21       POTENTIAL.
SQ   SEQUENCE   287 AA;  31927 MW;  [illegible] CRC64;

  Query Match          27.9%;  Score 105;  DB 1;  Length 287;
  Best Local Similarity   100.0%;  Pred. No. 0.0009;
  Matches  105;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      113 KPSLSAQPGP 122
            ||||||||||
Db      128 KPSLSAQPGP 137


RESULT 20
Q6N0I1
ID   Q6N0I1       PRELIMINARY;      PRT;   287 AA.
AC   Q6N0I1;
DT   01-MAY-2004 (TREMBLrel. 27, Created)
DT   01-MAY-2004 (TREMBLrel. 27, Last sequence update)
DT   01-DEC-2004 (TREMBLrel. 35, Last annotation update)
DE   NK receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euprimates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=23134786; PubMed=12777172;
RA   Kwon J., Shaw V.L., Shi L.Z., Park I.H., Kim S.J., Kim Y.;

RESULT 21
[illegible]
ID   [illegible]      PRELIMINARY;      PRT;   287 AA.
AC   [illegible];
DT   01-MAY-1997 (TREMBLrel. 03, Created)
DT   01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT   01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE   NK receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PERIPHERAL;
RA   Biassoni R.;
RL   Submitted (APR 1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X97232; CAA65784.1; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
SQ   SEQUENCE   287 AA;  [illegible] MW;  [illegible] CRC64;

  Query Match          27.9%;  Score 105;  DB 1;  Length 287;
  Best Local Similarity   100.0%;  Pred. No. 0.0009;
  Matches  105;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      113 KPSLSAQPGP 122
            ||||||||||
Db      128 KPSLSAQPGP 137


RESULT 22
Q6NAG1
ID   Q6NAG1       PRELIMINARY;      PRT;   287 AA.
AC   Q6NAG1;
DT   01-OCT-2004 (TREMBLrel. 27, Created)
DT   01-OCT-2004 (TREMBLrel. 27, Last sequence update)
DT   01-DEC-2004 (TREMBLrel. 35, Last annotation update)
DE   NK killer cell inhibitory receptor (fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euprimates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=23134786; PubMed=12777172;
RA   Kwon J., Shaw V.L., Shi L.Z., Park I.H., Kim S.J., Kim Y.;
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RT   "Diversity of the p70 killer cell inhibitory receptor (KIR2DL) fam...
RT   members in a single individual.";
RL   Mol. Cells 10:54-60(2000).
DR   EMBL; AF200866; AAF29517.1; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
KW   Receptor.
FT   NON_TER       1       1
FT   NON_TER     297     297
SQ   SEQUENCE   297 AA;  32748 MW;  E07AB1E3E3A6C7E7 CRC64;

  Query Match             2.9%;  Score 10;  DB 4;  Length 297;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      113 KPSLSAQPGP 122
            ||||||||||
Db      208 KPSLSAQPGP 217


RESULT 23
Q9NZD0
ID   Q9NZD0       PRELIMINARY;      PRT:   297 AA.
AC   Q9NZD0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   P70 killer cell inhibitory receptor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20234780; PubMed=10774747;
RA   Kwon S., Chwae Y.J., Choi I.H., Park I.H., Kim S.J., Kim J.;
RT   "Diversity of the p70 killer cell inhibitory receptor (KIR2DL) fam...
RT   members in a single individual.";
RL   Mol. Cells 10:54-60(2000).
DR   EMBL; AF200866; AAF29516.1; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
KW   Receptor.
FT   NON_TER       1       1
FT   NON_TER     297     297
SQ   SEQUENCE   297 AA;  32748 MW;  2D2DFB8428F5CA0F CRC64;

  Query Match             2.9%;  Score 10;  DB 4;  Length 297;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      113 KPSLSAQPGP 122
            ||||||||||
Db      208 KPSLSAQPGP 217


RESULT 24
Q9NZF8
ID   Q9NZF8       PRELIMINARY;      PRT:   297 AA.
AC   Q9NZF8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   P70 killer cell inhibitory receptor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20234780; PubMed=10774747;
RA   Kwon S., Chwae Y.J., Choi I.H., Park I.H., Kim S.J., Kim J.;
RT   "Diversity of the p70 killer cell inhibitory receptor (KIR2DL) fam...
RT   members in a single individual.";
RL   Mol. Cells 10:54-60(2000).
DR   EMBL; AF200866; AAF29518.1; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
KW   Receptor.
FT   NON_TER       1       1
FT   NON_TER     297     297
SQ   SEQUENCE   297 AA;  32649 MW;  5A2C8407C9F8EDB9 CRC64;

  Query Match             2.9%;  Score 10;  DB 4;  Length 297;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      113 KPSLSAQPGP 122
            ||||||||||
Db      208 KPSLSAQPGP 217


RESULT 25
Q9NZF7
ID   Q9NZF7       PRELIMINARY;      PRT:   297 AA.
AC   Q9NZF7;
```

```
LO   ..-..-2000 (IrEMBLrel. 15, Created)
DT   ..-..-2000 (IrEMBLrel. 15, Last sequence update)
DT   ..-DEC-2001 (IrEMBLrel. 19, Last annotation update)
DE   p70 killer cell inhibitory receptor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; ...
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; ...
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20234780; PubMed=10774747;
RA   Kwon J., Chung Y.J., Choi I.H., Park J.H., Kim S., ...
RT   "Diversity of the p70 killer cell inhibitory receptor ...
RT   members in a single individual.";
RL   Mol. Cells 10:54-60(2000).
DR   EMBL; AF208680; AAF24...; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
FT   NON_TER       1       1
FT   NON_TER     297     297
SQ   SEQUENCE   297 AA;  ...  MW;  ...

  Query Match          ...%;  Score ...;  DB 4;  Length 297;
  Best Local Similarity   ...%;  Pred. No. ...;
  Matches  ...;  Conservative  ...;  Mismatches  ...;  Indels  ...;  Gaps  ...;

Qy      ... KPSLSAQPGP 122
                ||||||||||
Db      262 KPSLSAQPGP 271


RESULT 27
Q9NZF5
ID   Q9NZF5       PRELIMINARY;      PRT;   297 AA.
AC   Q9NZF5;
DT   01-OCT-2000 (IrEMBLrel. 15, Created)
DT   01-OCT-2000 (IrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (IrEMBLrel. 19, Last annotation update)
DE   p70 killer cell inhibitory receptor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; ...
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20234780; PubMed=10774747;
RA   Kwon J., Chung Y.J., Choi I.H., Park J.H., Kim S., ...
RT   "Diversity of the p70 killer cell inhibitory ...
RT   members in a single individual.";
RL   Mol. Cells 10:54-60(2000).
DR   EMBL; AF208680; AAF24...; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
FT   NON_TER       1       1
FT   NON_TER     297     297
SQ   SEQUENCE   297 AA;  ...  MW;  ...

  Query Match          ...%;  Score ...;  DB 4;  Length 297;
  Best Local Similarity   ...%;  Pred. No. ...;
  Matches  ...;  Conservative  ...;  Mismatches  ...;  Indels  ...;  Gaps  ...;

Qy      ... KPSLSAQPGP 122
                ||||||||||
Db      262 KPSLSAQPGP 271


RESULT 28
Q9NZF5
ID   Q9NZF5       PRELIMINARY;      PRT;   297 AA.
AC   Q9NZF5;
DT   01-OCT-2000 (IrEMBLrel. 15, Created)
DT   01-OCT-2000 (IrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (IrEMBLrel. 19, Last annotation update)
DE   p70 killer cell inhibitory receptor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20234780; PubMed=10774747;
RA   Kwon J., Chung Y.J., Choi I.H., Park J.H., Kim S., Kim J.;
RT   "Diversity of the p70 killer cell inhibitory receptor (KIR...) family
RT   members in a single individual.";
RL   Mol. Cells 10:54-60(2000).
DR   EMBL; AF208680; AAF24...; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
FT   NON_TER       1       1
FT   NON_TER     297     297
SQ   SEQUENCE   297 AA;  ...  MW;  ...

  Query Match          ...%;  Score ...;  DB 4;  Length 297;
  Best Local Similarity   ...%;  Pred. No. ...;
  Matches  ...;  Conservative  ...;  Mismatches  ...;  Indels  ...;  Gaps  ...;

Qy      ... KPSLSAQPGP 122
                ||||||||||
Db      262 KPSLSAQPGP 271


RESULT 29
Q90UM5
ID   Q90UM5       PRELIMINARY;      PRT;   298 AA.
AC   Q90UM5;
DT   01-MAY-2003 (IrEMBLrel. 24, Created)
DT   01-MAY-2003 (IrEMBLrel. 24, Last sequence update)
DT   01-DEC-2003 (IrEMBLrel. 29, Last annotation update)
DE   NKAP 2a like protein (Fragment).
GN   KIR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=23120888; PubMed=12911179;
RA   Wilson M.J., Torkar M., Haude A.;
RT   "Genomic organization of a human killer cell inhibitory receptor
RT   gene.";
RL   Tissue Antigens 62:173-179(2003).
DR   EMBL; AY...; AAP51...; -.
DR   EMBL; AY...; AAP51...; -.
DR   EMBL; AY...; AAP51...; -.
DR   EMBL; AY...; AAP51...; -.
DR   EMBL; AY...; AAP51...; -.
DR   EMBL; AY...; AAP51...; -.
DR   EMBL; AY...; AAP51...; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
FT   NON_TER     298     298
```

```
Sq   Sequence  ??? AA;  ?,???? MW;  ????????????????????????????????;

  Query Match             ??.?%;  Score ??;  DB ?;  Length ??;
  Best Local Similarity   ???.?%;  Pred. No. ?.??;
  Matches  ??;  Conservative  ??;  Mismatches  ??;  Indels  ??;  Gaps  ??;

Qy      ??? KPSESAQPGP ???
            ||| |  ||
Db      ??? KPSESAIPGP ???


RESULT ??
????????
ID   ????????      PRELIMINARY;      PRT;   ??? AA.
AC   ??????;
DT   ??-???-???? (IrEMBLrel. ??, Created)
DT   ??-???-???? (IrEMBLrel. ??, Last sequence update)
DT   ??-???-???? (IrEMBLrel. ??, Last annotation update)
DE   NK receptor precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=????;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Chae J.H., Kim Y.M., Ahn J.M., Kim C.G., Kim S., Kim S.J., Park J.H.;
RT   "Genomic organization of novel genes encoded human Killer Inhibitory
RT   receptors.";
RL   Submitted (MAR ????) to the EMBL/GenBank/DDBJ databases.
RP   EMBL; AF???????; AAD?????.?; -.
DR   HSSP; P?????; 1NKR.
DR   InterPro; IPR???????; Ig.
DR   InterPro; IPR???????; Ig_MHC.
DR   Pfam; PF?????; Ig; 2.
DR   SMART; SM?????; IG; 1.
KW   Receptor; Signal.
FT   SIGNAL       1     21       POTENTIAL.
Sq   SEQUENCE   ??? AA;  ?????? MW;  ???????????????? CRC??;

  Query Match             ??.?%;  Score ??;  DB ?;  Length ??;
  Best Local Similarity   ???.?%;  Pred. No. ?.??;
  Matches  ??;  Conservative  ??;  Mismatches  ??;  Indels  ??;  Gaps  ??;

Qy      ??? KPSESAQPGP ???
            ||||||||||
Db      ??? KPSESAQPGP ???


RESULT ??
????????
ID   ????????      PRELIMINARY;      PRT;   ??? AA.
AC   ??????;
DT   ??-???-???? (IrEMBLrel. ??, Created)
DT   ??-???-???? (IrEMBLrel. ??, Last sequence update)
DT   ??-???-???? (IrEMBLrel. ??, Last annotation update)
DE   NK receptor activating NK receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=????;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE=????????; PubMed=????????;
RA   Bilasy N.F., Dessibie A., Mallaspina A., Cantoni C., Pende D.,
RA   Sivori S., Moretta L., Moretta A.;
RT   "Molecular analysis of position 70 in the putative ligand-
RT   binding region of human killer cell activating receptors.";
RL   Eur. J. Immunol. ???:????-????(????).
DR   EMBL; ??????; AAA?????.?; -.
DR   HSSP; P?????; 1NKR.
DR   InterPro; IPR???????; Ig.
DR   InterPro; IPR???????; Ig_like.
DR   InterPro; IPR???????; Ig_MHC.
DR   Pfam; PF?????; Ig; 2.
DR   SMART; SM?????; IG; 1.
DR   SMART; SM?????; I-set; 1.
KW   Receptor.
Sq   SEQUENCE   ??? AA;  ?????? MW;  ???????????????? CRC??;

  Query Match             ??.?%;  Score ??;  DB ?;  Length ???;
  Best Local Similarity   ???.?%;  Pred. No. ?.??;
  Matches  ???;  Conservative  ???;  Mismatches  ??;  Indels  ??;  Gaps  ??;

Qy      ??? KPSESAQPGP ???
            |||||.|||| |
Db      ??? KPSESAQPGP ???


RESULT ??
????????
ID   ????????      PRELIMINARY;      PRT;   ??? AA.
AC   ??????;
DT   ??-???-???? (IrEMBLrel. ??, Created)
DT   ??-???-???? (IrEMBLrel. ??, Last sequence update)
DT   ??-???-???? (IrEMBLrel. ??, Last annotation update)
DE   NK receptor KIR2DL1.
GN   KIR2DL1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=????;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
Db   Pfam; PF?????; Ig; 2.
Db   SMART; SM?????; IG; 1.
Db   SMART; SM?????; I-set; 1.
KW   Receptor.
Sq   SEQUENCE   ??? AA;  ?????? MW;  ???????????????? CRC??;

  Query Match             ??.?%;  Score ??;  DB ?;  Length ???;
  Best Local Similarity   ???.?%;  Pred. No. ?.??;
  Matches  ???;  Conservative  ??;  Mismatches  ??;  Indels  ??;  Gaps  ??;

Qy      ??? KPSESAQPGP ???
            |||||||||| |
Db      ??? KPSESAQPGP ???


RESULT ??
????????
ID   ????????      PRELIMINARY;      PRT;   ??? AA.
AC   ??????;
DT   ??-MAY-???? (IrEMBLrel. ??, Created)
DT   ??-MAY-???? (IrEMBLrel. ??, Last sequence update)
DT   ??-DEC-???? (IrEMBLrel. ??, Last annotation update)
DE   Killer inhibitory receptor ?? 2.3 (Fragment).
GN   KIR2DL23.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=????;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Chae J.H., Kim Y.M., Ahn J.M., Kim C.G., Kim S., Kim S.J., Park J.H.;
RT   "Genomic organization of novel genes encoded human Killer Inhibitory
RT   receptors.";
RL   Submitted (MAR ????) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF?????; AAD?????.?; -.
DR   sMMo; ??????; AAD?????.?; JOINED.
DR   EMBL; AF?????; AAD?????.?; JOINED.
DR   EMBL; AF?????; AAD?????.?; JOINED.
DR   HSSP; P?????; 1NKR.
DR   InterPro; IPR???????; Ig.
DR   InterPro; IPR???????; Ig_MHC.
DR   Pfam; PF?????; Ig; 2.
DR   SMART; SM?????; IG; 1.
KW   Receptor.
FT   NON_TER      1      1
Sq   SEQUENCE   ??? AA;  ?????  MW;  ????????????????  CRC??;

  Query Match             ??.?%;  Score ??;  DB ?;  Length ???;
  Best Local Similarity   ???.?%;  Pred. No. ?.??;
  Matches  ???;  Conservative  ??;  Mismatches  ??;  Indels  ??;  Gaps  ??;

Qy      ??? KPSESAQPGP ???
            |||||.|||| |||
Db      ??? KPSESAQPGP ???


RESULT ??
????????
ID   ????????      PRELIMINARY;      PRT;   ??? AA.
AC   ??????;
DT   ??-JUN-???? (IrEMBLrel. ??, Created)
DT   ??-JUN-???? (IrEMBLrel. ??, Last sequence update)
DT   ??-JUN-???? (IrEMBLrel. ??, Last annotation update)
DE   NK receptor KIR2DL1.
GN   KIR2DL1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=????;
RN   [1]
RP   SEQUENCE FROM N.A.
```

RX MEDLINE; [illegible] PubMed [illegible];
RA Mengucci K.L., Wilson R.L., Harden K.L., Miner [illegible]
RT "Evolution of NK receptors: a [illegible] and [illegible]
RT [illegible]";
RL Eur. J. Immunol. [illegible].
DR EMBL; AY[illegible] AAL82601.1; -.
KW Receptor.
SQ SEQUENCE [illegible] AA; [illegible] MW; [illegible] CRC64;

Query Match [illegible]; Score [illegible]; [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

QY [illegible] LWSAISGPIE 149
[illegible]
Db [illegible] LWSAISGPIE 134

RESULT 44
Q14944
ID Q14944 PRELIMINARY; PRT; 44 AA.
AC Q14944;
DT [illegible]-NOV-[illegible] (IrEMBLrel. 60, Created)
DT [illegible]-NOV-[illegible] (IrEMBLrel. 91, Last sequence update)
DT [illegible]-[illegible] (IrEMBLrel. 19, Last annotation update)
DE Nkat2a.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96270004; PubMed [illegible];
RA [illegible]., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer [illegible]";
RL Immunogenetics 44:222-230(1996).
DR EMBL; L76664; AAB36911.1; -.
DR HSSP; P43626; 1NKR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
SQ SEQUENCE 441 AA; 47[illegible] MW; [illegible] CRC64;

Query Match [illegible]; Score [illegible]; [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

QY [illegible] KPSISAQPGP 122
[illegible]
Db [illegible] KPSLSAQPGP 137

RESULT 45
Q14945
ID Q14945 PRELIMINARY; PRT; 441 AA.
AC Q14945;
DT [illegible]-NOV-[illegible] (IrEMBLrel. 60, Created)
DT [illegible]-NOV-[illegible] (IrEMBLrel. 91, Last sequence update)
DT [illegible]-[illegible] (IrEMBLrel. 19, Last annotation update)
DE Nkat2d.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96270004; PubMed [illegible];
RA [illegible]., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer [illegible]";
RL Immunogenetics 44:222-230(1996).
DR EMBL; L76663; AAB36910.1; -.
DR HSSP; P43626; 1NKR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
SQ SEQUENCE 441 AA; 47[illegible] MW; [illegible] CRC64;

Query Match [illegible]; Score [illegible]; [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

QY [illegible] KPSISAQPGP 122
[illegible]
Db [illegible] KPSLSAQPGP 137

RESULT 46
P78402
ID P78402 PRELIMINARY; PRT; 441 AA.
AC P78402;
DT [illegible]-MAY-1997 (IrEMBLrel. 43, Created)
DT [illegible] MAY 1997 (IrEMBLrel. 43, Last sequence update)
DT [illegible]-[illegible] (IrEMBLrel. 26, Last annotation update)
DE NK receptor.
GN KIR2DS5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97215299; PubMed [illegible];
RA Selakovich A., Shilling [illegible];
RT "Polymorphism and [illegible] variability of human killer [illegible]
RT receptors.";
RL Immunol. Rev. 155:183-196(1997).
DR EMBL; U73395; AAC[illegible];
DR HSSP; P43626; 1NKR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
SQ SEQUENCE [illegible] AA; [illegible] MW; [illegible] CRC64;

Query Match [illegible]; Score [illegible]; [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

QY [illegible] KPSLSAQPGP 122
[illegible]
Db [illegible] KPSLSAQPGP 137

RESULT 47
Q14949
ID Q14949 PRELIMINARY; PRT; 441 AA.
AC Q14949;
DT [illegible]-NOV-[illegible] (IrEMBLrel. 60, Created)
DT [illegible]-NOV-[illegible] (IrEMBLrel. 91, Last sequence update)
DT [illegible]-[illegible] (IrEMBLrel. 19, Last annotation update)
DE Nkat3 protein (fragment).
GN Nkat3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96270004; PubMed [illegible];
RA [illegible]., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer [illegible]";
RL Immunogenetics 44:222-230(1996).
DR EMBL; L76665; AAB36912.1; -.
DR HSSP; P43626; 1NKR.

```
ID   Interim; [illegible]; [illegible].
DR   Interim; [illegible]; [illegible] MHC.
DR   PFam; [illegible]; [illegible].
DR   SMART; SM00[illegible]; [illegible].
SQ   SEQUENCE   [illegible] AA;  [illegible] MW;  [illegible] CRC64;

  Query Match             [illegible]%;  Score [illegible];  DB 4;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy      [illegible] KPSLSAQPSP [illegible]
            [illegible]
Db      [illegible] KPSISAQPSP [illegible]


RESULT 38
[illegible]
ID   [illegible]      PRELIMINARY;      PRT;   382 AA.
AC   [illegible];
DT   01-JUN-[illegible] (IrEMBLrel. 06, Created)
DT   01-JUN-[illegible] (IrEMBLrel. 06, Last sequence update)
DT   [illegible]-[illegible] (IrEMBLrel. [illegible], Last annotation update)
DE   Natural killer cell receptor KIR3DS1 variant.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; [illegible]; PubMed [illegible];
RA   Vilches C., Parham P.;
RT   "KIR3DS1, a gene encoding an activating killer cell receptor
RT   [illegible]";
RL   [illegible]
DR   EMBL; AF[illegible], AAB[illegible].1; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR[illegible]; Ig.
DR   InterPro; IPR[illegible]; Ig_MHC.
DR   PFam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
KW   Receptor.
SQ   SEQUENCE   382 AA;  42447 MW;  [illegible] CRC64;

  Query Match             [illegible]%;  Score [illegible];  DB 4;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy      [illegible] KPSLSAQPSP [illegible]
            [illegible]
Db      223 KPSISAQPSP 232


RESULT 39
[illegible]
ID   [illegible]      PRELIMINARY;      PRT;   382 AA.
AC   [illegible];
DT   01-MAY-[illegible] (IrEMBLrel. 03, Created)
DT   01-MAY-[illegible] (IrEMBLrel. 03, Last sequence update)
DT   01-DEC-[illegible] (IrEMBLrel. [illegible], Last annotation update)
DE   NK receptor.
GN   KIR 3DS1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; [illegible]; PubMed [illegible];
RA   Selvakumar A., Steffens U., Lapet R.;
RT   "Polymorphism and domain variability of Killer cell inhibitory
RT   receptors.";
RL   Immunol. Rev. [illegible] (1997).
DR   EMBL; U[illegible], AA[illegible].1; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR[illegible]; Ig.
DR   InterPro; IPR[illegible]; Ig_MHC.
DR   PFam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
SQ   SEQUENCE   410 AA;  44928 MW;  [illegible] CRC64;

  Query Match             [illegible]%;  Score [illegible];  DB 4;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy      [illegible] KPSLSAQPSP [illegible]
            [illegible]
Db      223 KPSISAQPSP 232


RESULT 40
[illegible]
ID   [illegible]      PRELIMINARY;      PRT;   410 AA.
AC   [illegible];
DT   [illegible]-MAY-[illegible] (IrEMBLrel. [illegible], Created)
DT   [illegible]-MAY-[illegible] (IrEMBLrel. [illegible], Last sequence update)
```

```
DE   SEQUENCE FROM N.A.
RX   MEDLINE; [illegible]; PubMed [illegible];
RA   Selvakumar A., Steffens U., Lapet R.;
RT   "Polymorphism and domain variability of Killer cell inhibitory
RT   receptors.";
RL   Immunol. Rev. [illegible] (1997).
DR   EMBL; U[illegible], AA[illegible].1; -.
DR   HSSP; P43626; 1NKR.
DR   InterPro; IPR[illegible]; Ig.
DR   InterPro; IPR[illegible]; Ig_MHC.
DR   PFam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
KW   Receptor.
SQ   SEQUENCE   382 AA;  42461 MW;  [illegible] CRC64;

  Query Match             [illegible]%;  Score [illegible];  DB 4;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy      [illegible] KPSLSAQPSP [illegible]
            [illegible]
Db      223 KPSISAQPSP 232


RESULT 41
[illegible]
ID   [illegible]      PRELIMINARY;      PRT;   410 AA.
AC   [illegible];
DT   [illegible]-MAY-[illegible] (IrEMBLrel. [illegible], Created)
DT   01-MAY-[illegible] (IrEMBLrel. [illegible], Last sequence update)
```

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LO   Q14C87 2   I (InEMBLrel. xx, Last annotation update,
DE   Killer cell inhibitory receptor KIR3...
 S   Homo sapiens (Human).
 C   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 C   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 X   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96077348; PubMed=7590832;
RA   Parham M., Norman P.J., Abi-Rached L., Moesta A.K., Walter L.,
RT   "Use of polymorphism of killer cell immunoglobulin-like receptors and
RT   their ligands in the study of natural selection and HLA.";
RL   Exp. Clin. Immunol. 13:157-167(1996).
DR   EMBL; AF072116; AAC39276.1;
DR   EMBL; AF072117; AAC39277.1; JOINED.
DR   EMBL; AF072400; AAC39278.1; JOINED.
DR   EMBL; AF072401; AAC39279.1; JOINED.
DR   HSSP; P43626; INKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 1.
KW   Receptor.
SQ   SEQUENCE   411 AA;  44910 MW;  21F2B4D7B4FEEE5F CRC64;

  Query Match              2.9%;  Score 16;  DB 4;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 1.1E+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     114 KPSLSAIPGP 123
           ||||||||||
Db     223 KPSLSAIPGP 232


RESULT 12
Q14C87
ID   Q14C87      PRELIMINARY;      PRT;   123 AA.
AC   Q14C87;
DT   01-JAN-1998 (IrEMBLrel. 05, Created)
DT   01-JAN-1998 (IrEMBLrel. 05, Last sequence update)
DT   15-MAR-2002 (IrEMBLrel. 20, Last annotation update)
DE   Monocyte inhibitory receptor precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Xue C.L., Wang Z.G., Ji K.F.;
RT   "Molecular identification of a novel family of human Ig superfamily
RT   superfamily members that possess immunoreceptor tyrosine-based
RT   inhibitory motifs and homology to the mouse gp49B1 receptor.";
RT   receptor.";
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U97427; AAB66667.1; -.
DR   HSSP; P43626; INKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 3.
KW   Receptor; Signal.
FT   N-GLYCOSYLATION      1      4       POTENTIAL.
FT   SIGNAL               1      4       POTENTIAL.
FT   CHAIN                5    123       MONOCYTE INHIBITORY RECEPTOR.
SQ   SEQUENCE   123 AA;  13960 MW;  41D6F2A9B6E4E4B4 CRC64;

  Query Match              2.9%;  Score 16;  DB 4;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 1.1E+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     195 SQILEVVPSS 204
           ||||||||||
Db      92 SQILEVVPSS 101


RESULT 43
Q15762
ID   Q15762      PRELIMINARY;      PRT;   427 AA.
AC   Q15762;
DT   01-NOV-1998 (IrEMBLrel. 41, Created)
DT   01-NOV-1998 (IrEMBLrel. 41, Last sequence update)
DT   01-DEC-2001 (IrEMBLrel. 56, Last annotation update)
DE   Killer cell inhibitory receptor 3
GN   NKIR3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Baker E.A., D'Andrea G.M., Phillips J.H., Lanier L.L.;
RT   Chromosome Res. 4:521-...(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=95478065; PubMed=7591044;
RA   D'Andrea A., Chang C., Franz-Bacon K., McClanahan T., Phillips J.H.,
RA   Lanier L.L.;
RT   "Molecular cloning of NKB1. A natural killer cell receptor for HLA-B
RT   allotypes.";
RL   J. Immunol. 155:2408-2417(1995).
DR   EMBL; U33626; AAC23725.1; -.
DR   HSSP; P43626; INKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
SQ   SEQUENCE   427 AA;  ??(?) Da;  ????????2D2??5E5 CRC64;

  Query Match              2.9%;  Score 16;  DB 4;  Length 427;
  Best Local Similarity   ?.?%;  Pred. No. 3.2E+03;
  Matches   16;  Conservative    0;  Mismatches    ?;  Indels    ?;  Gaps    ?;

Qy     114 KPSLSAIPGP 123
           ||||||||||
Db     223 KPSLSAIPGP 232


RESULT 44
Q09563
ID   Q09563      PRELIMINARY;      PRT;   436 AA.
AC   Q09563;
DT   01-MAY-1997 (IrEMBLrel. 03, Created)
DT   01-MAY-1997 (IrEMBLrel. 03, Last sequence update)
DT   01-DEC-2001 (IrEMBLrel. 54, Last annotation update)
DE   NK receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Synovium;
RA   Blaschke R.;
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X97283; CAA65866.1; -.
DR   HSSP; P43626; INKR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_MHC.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
KW   Receptor.
SQ   SEQUENCE   436 AA;  47461 MW;  ????79D8EB64A4625 CRC64;

  Query Match              2.9%;  Score 16;  DB 4;  Length 436;
```

Best Local Similarity 100.0%; Pred. No. 0.0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSISAQISF 10
||||||||||
Db 224 KPSISAQISF 233

RESULT 15
Q96PD4
ID Q96PD4 PRELIMINARY; PRT; 240 AA.
AC Q96PD4;
DT 01-FEB-2002 (TrEMBLrel. 21, Created)
DT 01-FEB-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 24, Last annotation update)
DE NK receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bensussan A., Boumsell L., Carosella E., Versteeg S., Fries M.,
RA di Bonaventura C., Accame L., Bottino C., Moretta A., Moretta L.;
RT "The natural killer cell receptor specific for HLA-A allotypes: a
RT novel member of the p58/p70 family of inhibitory receptors that is
RT characterized by three immunoglobulin-like domains and is expressed
RT as a 140-kD disulphide-linked dimer.";
RL J. Exp. Med. 180:953-960(1994).
DR EMBL; X66956; CAA47022.1; -.
DR HSSP; P43626; 1NKR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 2.
KW Receptor.
SQ SEQUENCE 240 AA; 26417 MW; 7DD72777B5ABE6C CRC64;

Query Match 22.9%; Score 10; DB 4; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSISAQISF 10
||||||||||
Db 223 KPSISAQISF 232

RESULT 16
Q95IG6
ID Q95IG6 PRELIMINARY; PRT; 249 AA.
AC Q95IG6;
DT 01-JAN-2002 (TrEMBLrel. 20, Created)
DT 01-JAN-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Monocyte inhibitory receptor precursor
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Arpin C.P., Navickaite C., Austen K.F.;
RT "Molecular identification of a newer family of human immunoglobulin
RT superfamily members that possess immunoreceptor tyrosine-based
RT inhibitory motifs and homology to the mouse gp49B1 receptor.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC020666; AAH20666.1; -.
DR HSSP; P43626; 1NKR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_MHC.

DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
KW Receptor; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 249 MONOCYTE INHIBITORY RECEPTOR.
SQ SEQUENCE 249 AA; 27366 MW; B8CF4C4E3B0B9C4 CRC64;

Query Match 22.9%; Score 10; DB 4; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSISAQISF 10
||||||||||
Db 232 KPSISAQISF 241

RESULT 17
Q75QJ6
ID Q75QJ6 PRELIMINARY; PRT; 444 AA.
AC Q75QJ6;
DT 01-NOV-2003 (TrEMBLrel. 26, Created)
DT 01-NOV-2003 (TrEMBLrel. 26, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Leukocyte immunoglobulin like receptor 4.
GN LIR 4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Borges L., Hsu M.L., Fanger N., Kubin M., Cosman D.;
RL J. Immunol. 159:5192-5196(1997).
DR EMBL; AF025527; AAB87661.1; -.
DR HSSP; P43626; 1NKR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.
SQ SEQUENCE 444 AA; 47952 MW; 2AE3C61F8C49CFE CRC64;

Query Match 22.9%; Score 10; DB 4; Length 444;
Best Local Similarity 100.0%; Pred. No. 0.0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSISAQISF 10
||||||||||
Db 177 KPSISAQISF 186

RESULT 18
Q9GER2
ID Q9GER2 PRELIMINARY; PRT; 444 AA.
AC Q9GER2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 19, Last annotation update)
DE KIR3DL1 like natural killer cell receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99116146; PubMed=9864845;
RA Vyas Y., Solrakanu A., Stettnisch H., Jones E.;
RT "Multiple transcripts of the killer cell immunoglobulin-like receptor
RT family, KIR3DL1 (NKB1), are expressed by natural killer cells of a
RT single individual.";
RL Tissue Antigens 51:1-9(1998).
DR EMBL; AF054519; AAC83627.1; -.
DR HSSP; P43626; 1NKR.
DR InterPro; IPR003599; Ig.

Db InterPro: IPR[illegible]; Eq_MHC;
Db Pfam: PF [illegible]; Eq; 1;
Db SMART: SM [illegible]; Eq; 2;
KW Receptor;
SQ SEQUENCE [illegible] AA; [illegible] MW; [illegible]

Query Match [illegible]; Score [illegible]; DB 3; Length [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible]
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

Qy [illegible] KPSLSAQLNP 122
[illegible]
Db 223 KPSLSAQLNP 232

RESULT 49
Q9TEK1
ID Q9TEK1 PRELIMINARY; PRT; 111 AA.
AC Q9TEK1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE KIR3DL1 like natural killer cell receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=[illegible]; PubMed=9804843;
RA Vyas Y., Selvakumar A., Steffens G., Dupont B.;
RT "Multiple transcripts of the killer cell immunoglobulin-like [illegible]
RT family, KIR3DL1 (NKB1), are expressed by natural killer [illegible]
RT single individual.";
RL Tissue Antigens 52:518-529(1998).
DR EMBL; AF130411; AAD39928.1; -.
DR HSSP; P43626; 1NKR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 2.
KW Receptor.
SQ SEQUENCE 111 AA; 12579 MW; 611A0C62A2E1A0C0 CRC64;

Query Match [illegible]; Score [illegible]; DB 3; Length 111;
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible] KPSLSAQLNP 122
[illegible]
Db 223 KPSLSAQLNP 232

RESULT 50
Q9TEK0
ID Q9TEK0 PRELIMINARY; PRT; 111 AA.
AC Q9TEK0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE KIR3DL1 like natural killer cell receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=[illegible]; PubMed=9804843;
RA Vyas Y., Selvakumar A., Steffens G., Dupont B.;
RT "Multiple transcripts of the killer cell immunoglobulin-like [illegible]
RT family, KIR3DL1 (NKB1), are expressed by natural killer [illegible]
RT single individual.";
RL Tissue Antigens 52:518-529(1998).
DR EMBL; AF130411; AAD39927.1; -.
DR HSSP; P43626; 1NKR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 2.
KW Receptor.
SQ SEQUENCE 111 AA; 12579 MW; 9D2C1F92E272A0D0 CRC64;

Query Match [illegible]; Score [illegible]; DB 4; Length 111;
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible] KPSLSAQLNP 122
[illegible]
Db 223 KPSLSAQLNP 232

Search completed: December [illegible], 2002, 07:00:14
Job time : [illegible] secs

Mprotein protein search, using sw model

Run on: December 5, 2002, 07:06:54 ; Search time [illegible]
(without alignments)
[illegible] Million cell updates/sec

Title:
Perfect score:
Sequence:

Scoring table:
Xgap Ygap Gapext

Searched:

Word size:

Total number of hits satisfying chosen parameters:

Minimum DB seq length:
Maximum DB seq length:

Post-processing: Listing first % summaries

Database:

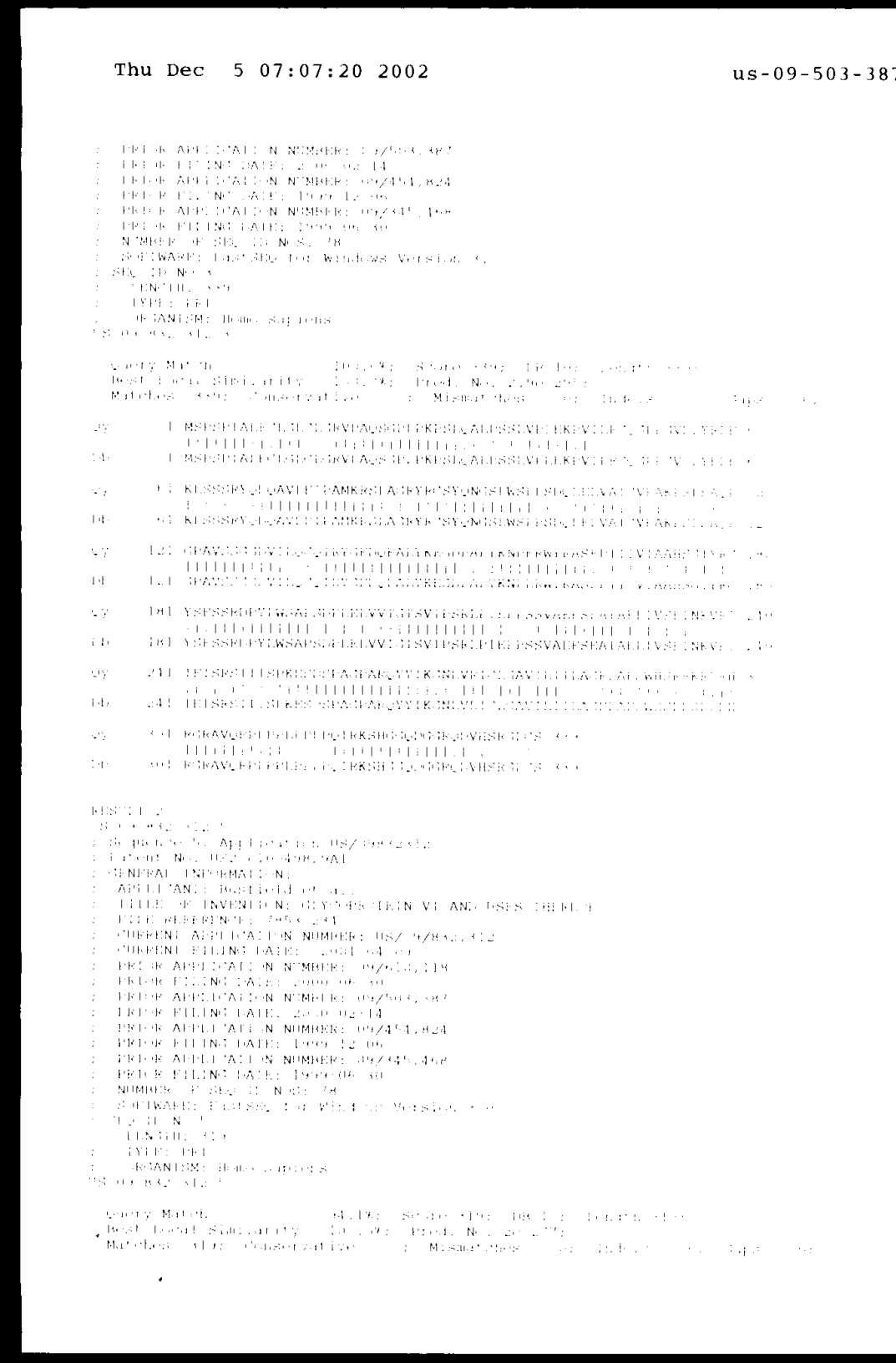
Prod. No. is the number of results predicted by random search
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

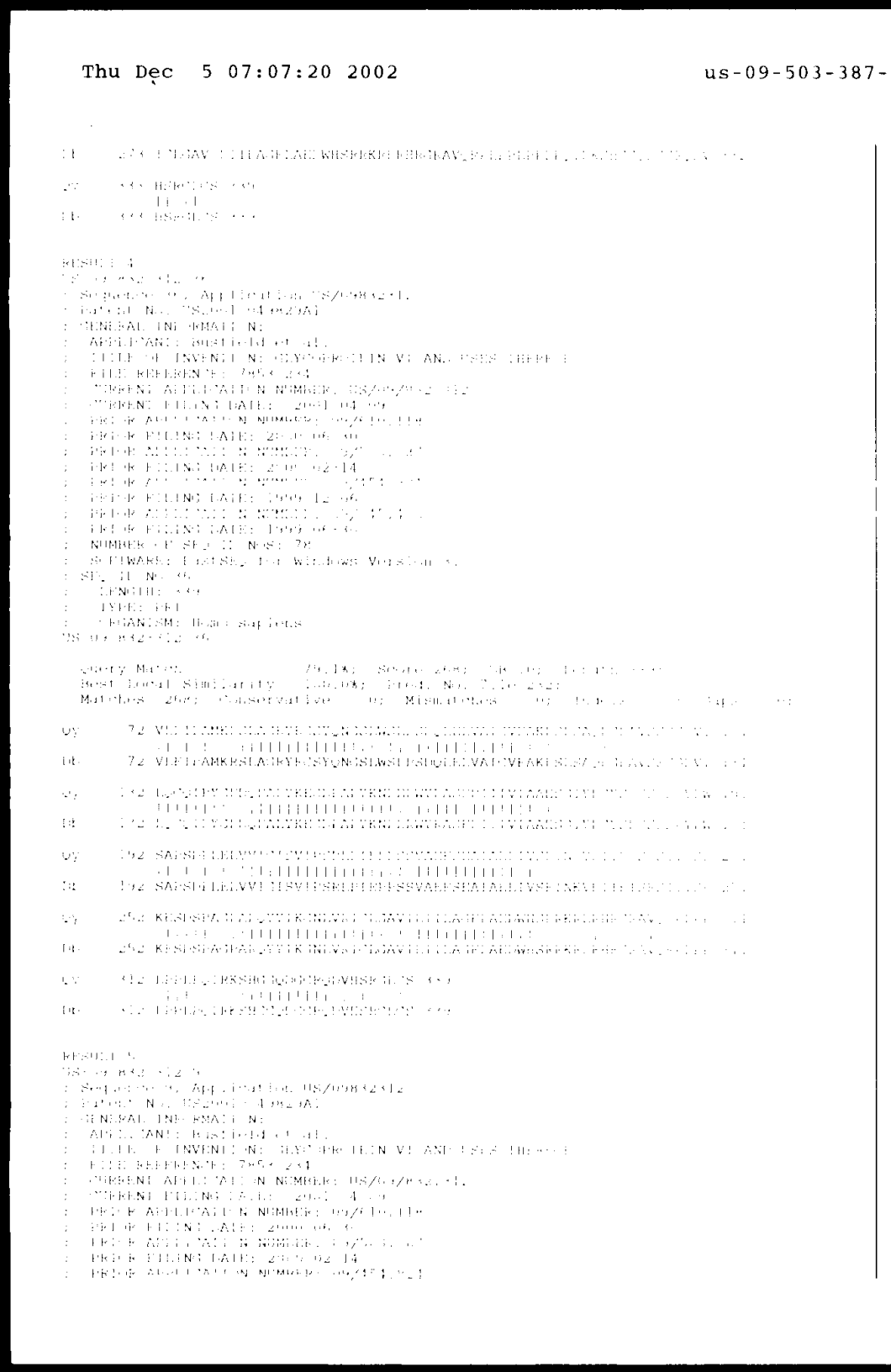
SUMMARIES

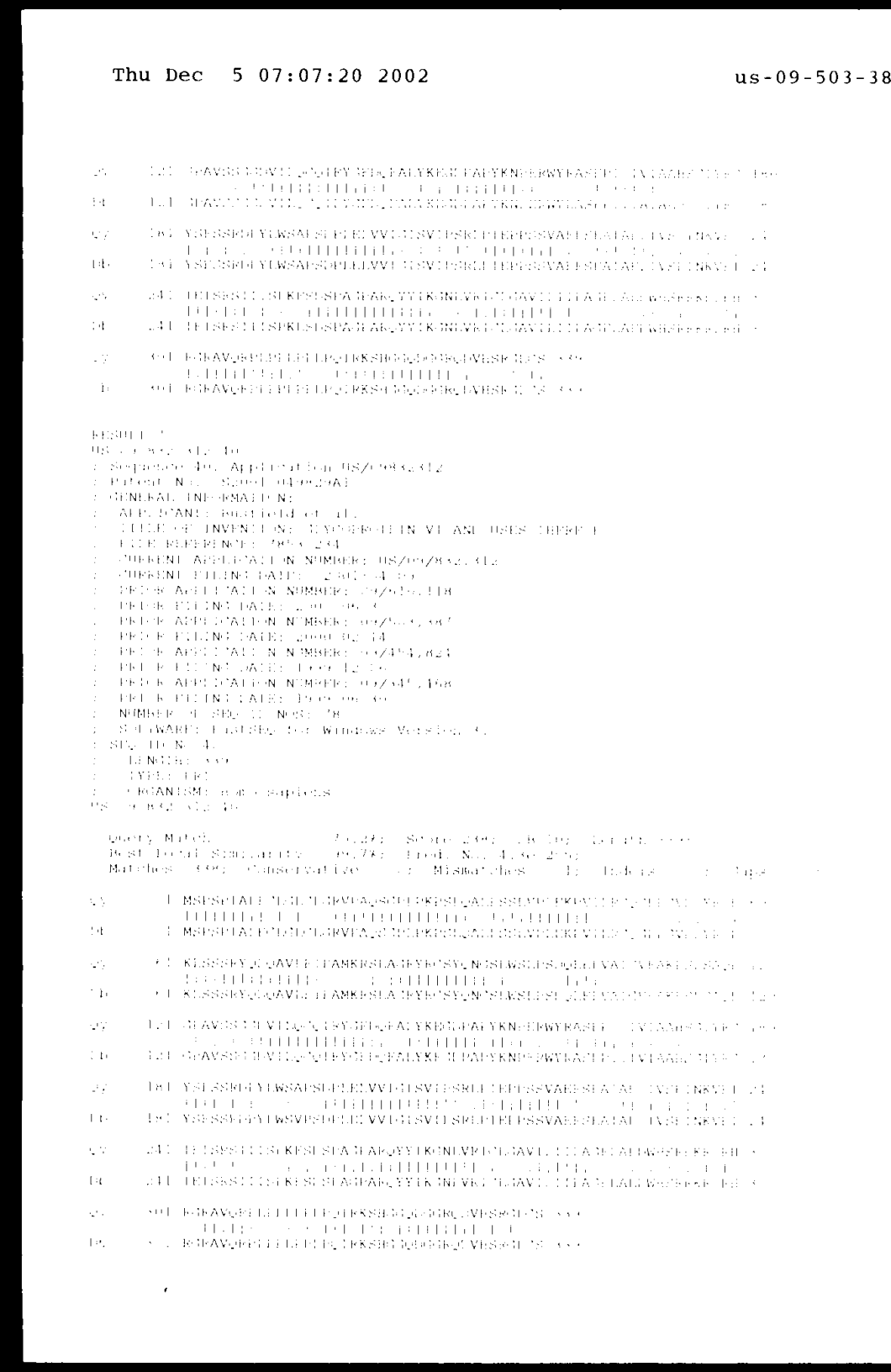
Result No.	Score	Query Match	Length	DB	ID	Description
1	339	100.0	339	10	US-09-832-512-3	Sequence 3, Appli
2	319	94.1	319	10	US-09-832-512-1	Sequence 1, Appli
3	307	90.6	339	10	US-09-832-512-34	Sequence 34, Appl
4	298	87.9	339	10	US-09-832-512-37	Sequence 37, Appl
5	244	72.0	244	10	US-09-832-512-2	Sequence 2, Appli
6	238	70.2	339	10	US-09-832-512-40	Sequence 40, Appl
7	238	70.2	339	10	US-09-832-512-41	Sequence 41, Appl
8	51	15.0	51	10	US-09-832-512-1	Sequence 1, Appli
9	47	13.9	47	10	US-09-832-512-7	Sequence 7, Appli
10	41	12.1	41	10	US-09-832-512-6	Sequence 6, Appli
11	27	8.0	267	10	US-09-832-512-19	Sequence 19, Appl
12	25	7.4	242	10	US-09-832-512-38	Sequence 38, Appl
13	25	7.4	313	10	US-09-832-512-15	Sequence 15, Appl
14	25	7.4	314	10	US-09-832-512-52	Sequence 52, Appl
15	25	7.4	314	10	US-09-832-512-44	Sequence 44, Appl
16	25	7.4	314	10	US-09-832-512-47	Sequence 47, Appl
17	25	7.4	314	10	US-09-832-512-48	Sequence 48, Appl
18	23	6.8	29	12	US-10-012-452-4	Sequence 4, Appli
19	19	5.6	19	10	US-09-832-512-8	Sequence 8, Appli
20	19	5.6	42	10	US-09-832-512-28	Sequence 28, Appl
21	19	5.6	42	10	US-09-870-957-48	Sequence 48, Appl
22	19	5.6	450	4	US-09-964-807-12	Sequence 12, Appl
23	19	5.6	41	10	US-09-832-512-22	Sequence 22, Appl
24	19	5.6	51	10	US-09-832-512-15	Sequence 15, Appl
25	19	5.6	86	10	US-09-864-761-66[illegible]	Sequence [illegible] A
26	19	5.6	1[illegible]	10	US-09-864-761-[illegible]	Sequence [illegible] A
27	19	5.6	13[illegible]	10	US-09-864-761-[illegible]	Sequence [illegible] A
28	19	5.6	1[illegible]	10	US-09-864-761-41[illegible]	Sequence 41[illegible] A
29	19	5.6	19[illegible]	10	US-09-832-512-26	Sequence 26, Appl
30	19	5.6	2[illegible]	10	US-09-832-512-27	Sequence 27, Appl
31	19	5.6	76[illegible]	10	US-09-864-761-45[illegible]	Sequence [illegible] A
32	19	5.6	89[illegible]	10	US-09-864-761-[illegible]	Sequence [illegible] A
33	19	5.6	457[illegible]	10	US-09-870-957-50	Sequence 50, Appl
34	19	5.6	19[illegible]	10	US-09-832-512-12	Sequence 12, Appl
35	19	5.6	[illegible]	10	US-09-964-679-4	Sequence 4, Appli
36	19	5.6	[illegible]	10	US-09-870-957-45	Sequence 45, Appl
37	19	5.6	[illegible]	10	US-09-938-525-6	Sequence 6, Appli
38	19	5.6	[illegible]	10	US-09-938-525-12	Sequence 12, Appl
39	19	5.6	13[illegible]	10	US-09-870-957-179	Sequence 179, App
40	19	5.6	14[illegible]	10	US-09-938-525-62	Sequence 62, Appl
41	19	5.6	15[illegible]	10	US-09-880-152-16	Sequence 16, Appl
42	19	5.6	15[illegible]	10	US-09-870-957-147	Sequence 147, App
43	19	5.6	15[illegible]	10	US-09-890-119-76	Sequence 76, Appl
44	19	5.6	15[illegible]	10	US-09-870-957-156	Sequence 156, App
45	19	5.6	15[illegible]	10	US-09-870-957-148	Sequence 148, App
46	19	5.6	[illegible]	10	US-09-759-143-[illegible]	Sequence [illegible] App
47	19	5.6	21[illegible]	10	US-09-780-[illegible]	Sequence [illegible] App
48	19	5.6	[illegible]	10	US-09-822-427-[illegible]	Sequence [illegible] App
49	19	5.6	[illegible]	9	US-09-970-008-202	Sequence 202, App
50	19	5.6	[illegible]	10	US-09-870-[illegible]-202	Sequence 202, App
51	19	5.6	[illegible]	10	US-09-870-523-21	Sequence 21, App
52	19	5.6	[illegible]	10	US-09-864-761-40[illegible]	Sequence 4[illegible] A
53	19	5.6	[illegible]	10	US-09-864-761-41[illegible]	Sequence 41[illegible] A
54	19	5.6	[illegible]	10	US-09-864-761-45[illegible]	Sequence 45[illegible] A
55	19	5.6	[illegible]	10	US-09-864-761-47[illegible]	Sequence 47[illegible] A
56	19	5.6	[illegible]	10	US-09-864-761-47[illegible]	Sequence 1748, A
57	19	5.6	[illegible]	10	US-09-864-761-48[illegible]	Sequence 48[illegible] A
58	19	5.6	[illegible]	10	US-09-864-761-41[illegible]	Sequence 41[illegible] A
59	19	5.6	1[illegible]	10	US-09-964-[illegible]-[illegible]	Sequence [illegible] A
60	19	5.6	11[illegible]	10	US-09-251-879-5	Sequence 5, Appli
61	19	5.6	11[illegible]	10	US-09-815-[illegible]-5	Sequence 5, Appli
62	19	5.6	11[illegible]	10	US-09-[illegible]-[illegible]	Sequence [illegible] Appl
63	19	5.6	12[illegible]	10	US-09-[illegible]-[illegible]	Sequence [illegible] Appl
64	19	5.6	14[illegible]	10	US-09-872-523-29	Sequence 29, Appl
65	19	5.6	14[illegible]	10	US-09-872-523-[illegible]	Sequence 45, Appl
66	19	5.6	29[illegible]	12	US-10-052-586-544	Sequence 544, App
67	19	5.6	27[illegible]	10	US-09-872-523-41	Sequence 41, App
68	19	5.6	241[illegible]	8	US-08-971-817A-6	Sequence 6, Appli
69	19	5.6	25[illegible]	10	US-09-802-[illegible]-25	Sequence 25, Appl
70	19	5.6	28[illegible]	10	US-09-193-[illegible]-6	Sequence 6, Appli
71	19	5.6	28[illegible]	10	US-09-027-[illegible]-6	Sequence 6, Appli
72	19	5.6	28[illegible]	10	US-09-252-[illegible]-7	Sequence 7, Appli
73	19	5.6	28[illegible]	10	US-09-929-[illegible]-6	Sequence 6, Appli
74	19	5.6	28[illegible]	10	US-09-927-[illegible]-1	Sequence 1, Appli
75	19	5.6	28[illegible]	12	US-10-012-452-[illegible]	Sequence [illegible] App

ALIGNMENTS

RESULT 1
US-09-832-512-3
; Sequence 3, Application US/09/832,512
; Patent No. US20010049826A1
; GENERAL INFORMATION:
; APPLICANT: Bostick, et al.
; TITLE OF INVENTION: SLY1 POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 7053.2x4
; CURRENT APPLICATION NUMBER: US/09/832,512
; CURRENT FILING DATE: 2001-04-[illegible]
; PRIOR APPLICATION NUMBER: 60/[illegible],18
; PRIOR FILING DATE: 2000-04-20







RESULT 8
US/09/892,412
; Sequence 10, Application US/09892412
; Patent No. US20020028449
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7959.234
; CURRENT APPLICATION NUMBER: US/09/892,412
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/651,118
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/253,887
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/244,824
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 60/244,488
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US/09/892,412-10

Query Match 75.0%; Score 15; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 CAAHSPKKKGKHPGKAV 220
||||||||||||||||| |
Db 1 CAAHSPKKKGKHPGKAV 17

RESULT 9
US/09/892,412/7
; Sequence 7, Application US/09892412
; Patent No. US20020028449
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7959.234
; CURRENT APPLICATION NUMBER: US/09/892,412
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/651,118
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/253,887
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/244,824
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 60/244,488
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo sapiens
US/09/892,412-7

Query Match 14.0%; Score 4; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 164 CQIRYSEGQFALYAFSGAIYENEFWYRASFFKLVIAAHSGIYRC 209
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 CQIRYSEGQFALYAFSGAIYENEFWYRASFFKLVIAAHSGIYRC 47

RESULT 10
US/09/892,412/6
; Sequence 6, Application US/09892412

; Patent No. US6010829A1
; GENERAL INFORMATION:
; APPLICANT: Bostick et al.
; TITLE OF INVENTION: GLY PROTEIN V, AND USES THERE
; FILE REFERENCE: 7853.234
; CURRENT APPLICATION NUMBER: US/09/503,387
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/010,116
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 08/785,987
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: 08/454,824
; PRIOR FILING DATE: 1995-05-30
; PRIOR APPLICATION NUMBER: 08/445,418
; PRIOR FILING DATE: 1995-05-30
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-503-387-3

Query Match 12.1%; Score 11; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 QQGPPQVSIYPLEKGSSSKYQQQAVETYAMKESLAKYP 50
|||||||||||
Db 1 QQGPPQVSIYPLEKGSSSKYQQQAVETYAMKESLAKYP 41

RESULT 11
US-09-503-387-3 ID
; Sequence 3, Application US/09503387
; Patent No. US6010829A1
; GENERAL INFORMATION:
; APPLICANT: Bostick et al.
; TITLE OF INVENTION: GLYCOPROTEIN V, AND USES THERE
; FILE REFERENCE: 7853.234
; CURRENT APPLICATION NUMBER: US/09/503,387
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/010,116
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 08/785,987
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: 08/454,824
; PRIOR FILING DATE: 1995-05-30
; PRIOR APPLICATION NUMBER: 08/445,418
; PRIOR FILING DATE: 1995-05-30
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-503-387-3

Query Match 12.1%; Score 11; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 QQGPPQVSIYPLEKGSSSKYQQQAVETYAMKESLAKYP 50
|||||||||||
Db 1 QQGPPQVSIYPLEKGSSSKYQQQAVETYAMKESLAKYP 41

RESULT 12
US-09-503-387-3
; Sequence 3, Application US/09503387
; Patent No. US6010829A1
; GENERAL INFORMATION:
; APPLICANT: Bostick et al.
; TITLE OF INVENTION: GLYCOPROTEIN V, AND USES THERE
; FILE REFERENCE: 7853.234
; CURRENT APPLICATION NUMBER: US/09/503,387
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/010,116
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 08/785,987
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: 08/454,824
; PRIOR FILING DATE: 1995-05-30
; PRIOR APPLICATION NUMBER: 08/445,418
; PRIOR FILING DATE: 1995-05-30
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-503-387-3

Query Match 12.1%; Score 11; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 QQGPPQVSIYPLEKGSSSKYQQQAVETYAMKESLAKYP 50
|||||||||||
Db 1 QQGPPQVSIYPLEKGSSSKYQQQAVETYAMKESLAKYP 41

RESULT 13
US-09-503-387-3
; Sequence 3, Application US/09503387
; Patent No. US6010829A1
; GENERAL INFORMATION:
; APPLICANT: Bostick et al.
; TITLE OF INVENTION: GLYCOPROTEIN V, AND USES THERE
; FILE REFERENCE: 7853.234
; CURRENT APPLICATION NUMBER: US/09/503,387
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/010,116
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 08/785,987
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: 08/454,824
; PRIOR FILING DATE: 1995-05-30
; PRIOR APPLICATION NUMBER: 08/445,418
; PRIOR FILING DATE: 1995-05-30
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-503-387-3

Query Match 12.1%; Score 11; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 QQGPPQVSIYPLEKGSSSKYQQQAVETYAMKESLAKYP 50
|||||||||||
Db 1 QQGPPQVSIYPLEKGSSSKYQQQAVETYAMKESLAKYP 41

RESULT 14
US-09-503-387-3
; Sequence 3, Application US/09503387
; Patent No. US6010829A1
; GENERAL INFORMATION:
; APPLICANT: Bostick et al.
; TITLE OF INVENTION: GLYCOPROTEIN V, AND USES THERE
; FILE REFERENCE: 7853.234
; CURRENT APPLICATION NUMBER: US/09/503,387

; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/615,119
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/414,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,409
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-863-412-42

Query Match 7.2%; Score 21; DB 6; Length 458;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 EFCIVIAARSCIYPCYSPESS 126
||||||||||||||||||||
Db 196 EFCIVIAARSCIYPCYSPESS 216

RESULT 7
US-09-863-412-43
; Sequence 43, Application US/09863412
; Patent No. US20010049429A1
; GENERAL INFORMATION:
; APPLICANT: Bostwick Hartzell et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 785.234
; CURRENT APPLICATION NUMBER: US/09/863,412
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/615,119
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/414,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,409
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-863-412-43

Query Match 7.2%; Score 21; DB 6; Length 458;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 EFCIVIAARSCIYPCYSPESS 126
||||||||||||||||||||
Db 196 EFCIVIAARSCIYPCYSPESS 216

RESULT 8
US-09-863-412-44
; Sequence 44, Application US/09863412
; Patent No. US20010049429A1
; GENERAL INFORMATION:
; APPLICANT: Bostwick Hartzell et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 785.234
; CURRENT APPLICATION NUMBER: US/09/863,412
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/615,119
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/414,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,409
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-863-412-44

Query Match 7.2%; Score 21; DB 6; Length 458;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 EFCIVIAARSCIYPCYSPESS 126
||||||||||||||||||||
Db 196 EFCIVIAARSCIYPCYSPESS 216

RESULT 9
US-09-863-412-45
; Sequence 45, Application US/09863412
; Patent No. US20010049429A1
; GENERAL INFORMATION:
; APPLICANT: Bostwick Hartzell et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 785.234
; CURRENT APPLICATION NUMBER: US/09/863,412
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/615,119
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/414,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,409
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-863-412-45

Query Match 7.2%; Score 21; DB 6; Length 458;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 EFCIVIAARSCIYPCYSPESS 126
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Db 196 EFCIVIAARSCIYPCYSPESS 216

RESULT 10
US-09-863-412-46
; Sequence 46, Application US/09863412
; Patent No. US20010049429A1
; GENERAL INFORMATION:
; APPLICANT: Bostwick Hartzell et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 785.234
; CURRENT APPLICATION NUMBER: US/09/863,412
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/615,119
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/414,824

; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/455,169
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-503-387-4

Query Match 0.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCTCCATCAGTCCTGCTCA 20
||||||||||||||||||||
Db 1 GTCTCCATCAGTCCTGCTCA 20

RESULT 10
US-09-503-387-5
; Sequence 5, Application US/09503387
; Patent No. US20020086291A1
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Walter F. et al.
; TITLE OF INVENTION: POLYMORPHISM IN VT AND USES THEREOF
; FILE REFERENCE: 7855-241
; CURRENT APPLICATION NUMBER: US/09/503,387
; CURRENT FILING DATE: 2000-04-09
; PRIOR APPLICATION NUMBER: US 09/455,169
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/455,169
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US/09/455,634
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,469
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-503-387-5

Query Match 95.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTCTCCATCAGTCCTGCTC 20
||||||||||||||||||||
Db 1 GTCTCCATCAGTCCTGCTC 19

RESULT 20
US-09-503-387-24
; Sequence 24, Application US/09503387
; Patent No. US20020086291A1
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Walter F. et al.
; TITLE OF INVENTION: POLYMORPHISM IN VT AND USES THEREOF
; FILE REFERENCE: 7855-241
; CURRENT APPLICATION NUMBER: US/09/503,387
; CURRENT FILING DATE: 2000-04-09
; PRIOR APPLICATION NUMBER: US/09/455,169
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US/09/455,634
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,469
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-503-387-24

Query Match 95.0%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCTCCATCAGTCCTGCTC 19
||||||||||||||||||||
Db 2 GTCTCCATCAGTCCTGCTC 20

RESULT 21
US-09-503-387-25
; Sequence 25, Application US/09503387
; Patent No. US20020086291A1
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Walter F. et al.
; TITLE OF INVENTION: POLYMORPHISM IN VT AND USES THEREOF
; FILE REFERENCE: 7855-241
; CURRENT APPLICATION NUMBER: US/09/503,387
; CURRENT FILING DATE: 2000-04-09
; PRIOR APPLICATION NUMBER: US/09/455,169
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US/09/455,634
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,469
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-503-387-25

Query Match 95.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTCTCCATCAGTCCTGCTC 20
||||||||||||||||||||
Db 1 GTCTCCATCAGTCCTGCTC 19

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-503-387-23

Query Match 85.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCTCCATCAGTCCTGC 17
|||||||||||||||||
Db 2 GTCTCCATCAGTCCTGC 18

RESULT 11
US-09-503-387-18
; Sequence 18, Application US/09503387
; Patent No. US20020177755A1
; GENERAL INFORMATION:
; APPLICANT: ELEMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING SLE ASSOCIATED
; FILE REFERENCE: 870254
; CURRENT APPLICATION NUMBER: US/09/503,387
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/128,128
; PRIOR FILING DATE: 2000-04-30
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 410
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-870-254-18

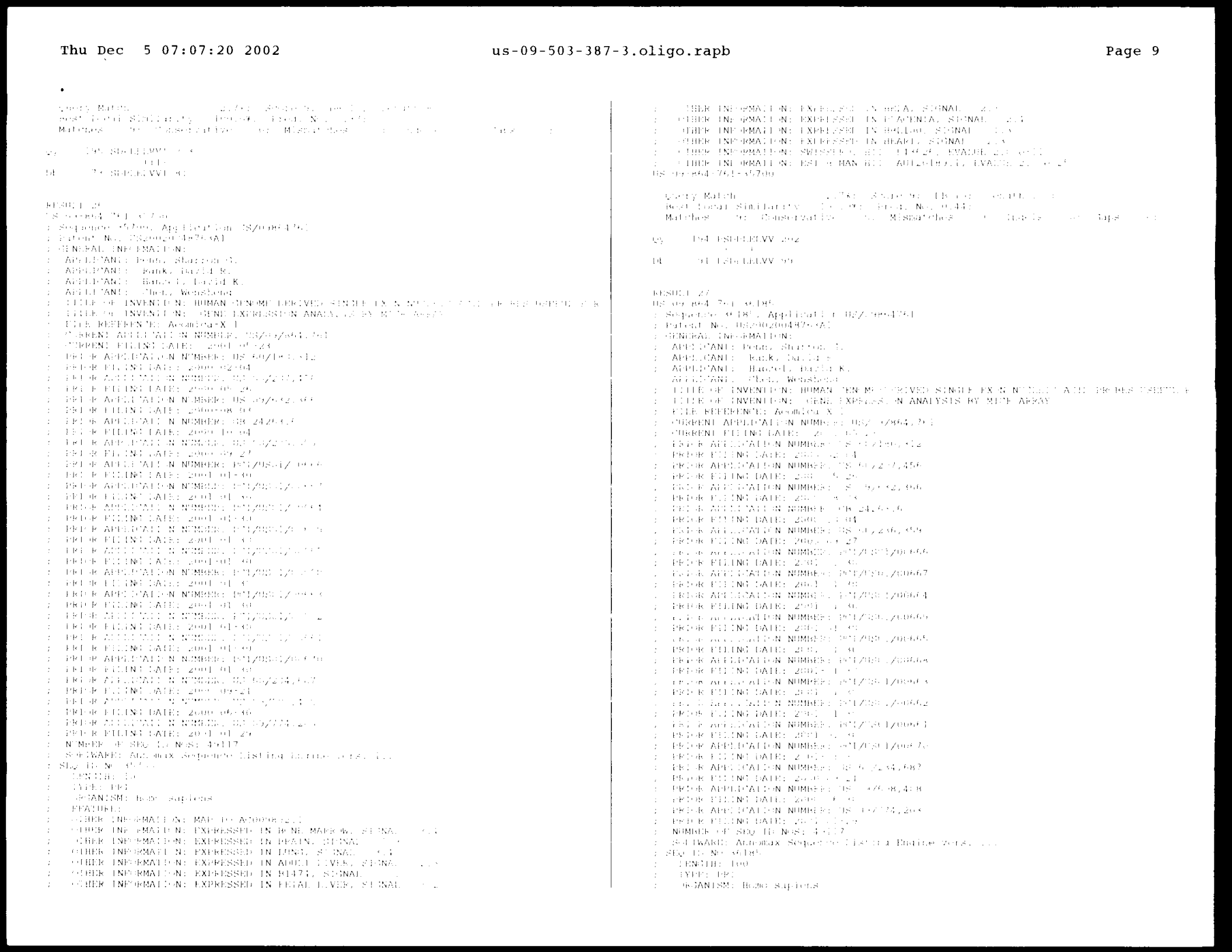
Query Match 21.4%; Score 19; DB 1; Length 410;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 GTCTCCATCAGTCCTGCTC 132
||||||||||||||||||||
Db 223 GTCTCCATCAGTCCTGCTC 241

RESULT 12
US-09-944-807-12
; Sequence 12, Application US/09944807
; Patent No. US20020119404A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which specifically
; TITLE OF INVENTION: Pulmonary inflammatory conditions and COPD
; TITLE OF INVENTION: Pulmonary airway diseases
; FILE REFERENCE: 0827.0P
; CURRENT APPLICATION NUMBER: US/09/944,807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: DE 100 41 [illegible]
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-944-807-12

Query Match 21.4%; Score 19; DB 1; Length 465;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 GTCTCCATCAGTCCTGCTC 213



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;  FEATURE:
;    OTHER INFORMATION: MAP To AC000812.2
;    OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL    4.4
;    OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL    2.
;    OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL    2.0
;    OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL    2.0
;    OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL    11
;    OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL    2.0
;    OTHER INFORMATION: EXPRESSED IN BETA, SIGNAL    2.
;    OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL    2.3
;    OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL    2.0
;    OTHER INFORMATION: SWISSPROT HIT: P14020, EVALUE 1.e-17
;    OTHER INFORMATION: EST HUMAN HIT: AW127890.1, EVALUE 1.e-50
US-09-503-387-3

  Query Match              2.4%;  Score 82;  DB 1;  Length 1;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCCCGGGCCCGGG 15
          |||||||||||||||
Db      1 GGGCCCGGGCCCGGG 15


RESULT 29
US-09-503-387-3
; Sequence 3, Application US/09503387
; Patent No. US20020164829A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G
;  APPLICANT: Banks, David K.
;  APPLICANT: Hunter, David K.
;  APPLICANT: Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME DERIVED SINGLE EXONS AND ...
;  TITLE OF INVENTION: GENE EXPRESSED IN ANALYSIS OF MICROARRAY
;  FILE REFERENCE: Assignee X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/206,312
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/852,806
;  PRIOR FILING DATE: 2001-05-24
;  PRIOR APPLICATION NUMBER: GB 212.3.6
;  PRIOR FILING DATE: 2000-12-04
;  PRIOR APPLICATION NUMBER: US 60/236,419
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00000
;  PRIOR FILING DATE: 2001-01-00
;  PRIOR APPLICATION NUMBER: PCT/US01/00002
;  PRIOR FILING DATE: 2001-01-00
;  PRIOR APPLICATION NUMBER: PCT/US01/00004
;  PRIOR FILING DATE: 2001-01-00
;  PRIOR APPLICATION NUMBER: PCT/US01/00003
;  PRIOR FILING DATE: 2001-01-00
;  PRIOR APPLICATION NUMBER: PCT/US01/00005
;  PRIOR FILING DATE: 2001-01-00
;  PRIOR APPLICATION NUMBER: PCT/US01/00008
;  PRIOR FILING DATE: 2001-01-00
;  PRIOR APPLICATION NUMBER: PCT/US01/00006
;  PRIOR FILING DATE: 2001-01-00
;  PRIOR APPLICATION NUMBER: PCT/US01/00007
;  PRIOR FILING DATE: 2001-01-00
;  PRIOR APPLICATION NUMBER: PCT/US01/00009
;  PRIOR FILING DATE: 2001-01-00
;  PRIOR APPLICATION NUMBER: US 09/851,687
;  PRIOR FILING DATE: 2001-05-09
;  PRIOR APPLICATION NUMBER: US 09/908,308
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 09/921,227
;  PRIOR FILING DATE: 2001-08-03
;  NUMBER OF SEQ ID NOS: 4317
;  SOFTWARE: Microsoft Sequence Listing Editor Ver. 1.1
; SEQ ID NO 3
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP To AC091127.3
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL    4.4
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL    2.0
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL    2.0
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL    2.0
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL    2.0
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL    2.0
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL    2.0
;   OTHER INFORMATION: SWISSPROT HIT: P14020, EVALUE 1.0e-16
;   OTHER INFORMATION: EST HUMAN HIT: AW127890.1, EVALUE 1.0e-50
US-09-503-387-3

  Query Match              2.4%;  Score 82;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCCCGGGCCCGGG 15
          |||||||||||||||
Db      1 GGGCCCGGGCCCGGG 15


RESULT 29
US-09-503-387-3
; Sequence 29, Application US/09503387
; Patent No. US20020164829A1
; GENERAL INFORMATION:
;  APPLICANT: Bostwick et al.
;  TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
;  FILE REFERENCE: 7854-234
;  CURRENT APPLICATION NUMBER: US/09/503,387
;  CURRENT FILING DATE: 2001-04-09
;  PRIOR APPLICATION NUMBER: 09/610,118
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: 09/503,887
;  PRIOR FILING DATE: 2000-02-14
;  PRIOR APPLICATION NUMBER: 09/454,921
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 09/435,854
;  PRIOR FILING DATE: 1999-11-05
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn for Windows Version 3.1
; SEQ ID NO 2
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-503-387-3

  Query Match              2.4%;  Score 82;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCCCGGGCCCGGG 15
          |||||||||||||||
Db      1 GGGCCCGGGCCCGGG 15


RESULT 30
US-09-503-387-21
; Sequence 21, Application US/09503387
; Patent No. US20020164829A1
; GENERAL INFORMATION:
;  APPLICANT: Bostwick et al.
;  TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
;  FILE REFERENCE: 7854-234
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;  CURRENT APPLICATION NUMBER: US/09/8[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 09/[illegible],118
;  PRIOR FILING DATE: 20[illegible]
;  PRIOR APPLICATION NUMBER: 09/503,387
;  PRIOR FILING DATE: 2000-02-14
;  PRIOR APPLICATION NUMBER: 09/154,824
;  PRIOR FILING DATE: 1998-12-16
;  PRIOR APPLICATION NUMBER: 09/345,168
;  PRIOR FILING DATE: 1999-06-30
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 27
;   TYPE: [illegible]
;   ORGANISM: Mus musculus
US-09-842-812-21

  Query Match             2.4%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy        [illegible] LRHHHLP 313
              [illegible]
Db          [illegible] LRHHHLP 2[illegible]


RESULT 41
US-09-864-761-45428
; Sequence 45428, Application US/09864761
; Patent No. US2002004876[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24[illegible]
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/[illegible],408
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: 2001-[illegible]-29
;  NUMBER OF SEQ ID NOS: 4[illegible]
;  SOFTWARE: Aeomica Sequence Listing Engine vers. 1.1
; SEQ ID NO 45428
;   LENGTH: 76
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC[illegible]
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL [illegible]
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL [illegible]
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL [illegible]
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL [illegible]
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL [illegible]
;   OTHER INFORMATION: EXPRESSED IN [illegible], SIGNAL [illegible]
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL [illegible]
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL [illegible]
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL [illegible]
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL [illegible]
;   OTHER INFORMATION: EST HUMAN HIT: AU1[illegible], EVALUE [illegible]
;   OTHER INFORMATION: SWISSPROT HIT: P4[illegible], EVALUE [illegible]
US-09-864-761-45428

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length 76;
  Best Local Similarity   [illegible];  Pred. No. 2.7[illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy        [illegible] WSALSDRL 108
              [illegible]
Db         64 WSALSDRL 71


RESULT 42
US-09-864-761-48160
; Sequence 48160, Application US/09864761
; Patent No. US2002004876[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  [illegible]
;  PRIOR APPLICATION NUMBER: US 60/[illegible],312
;  PRIOR FILING DATE: [illegible]-04
;  PRIOR APPLICATION NUMBER: US 60/[illegible],456
;  PRIOR FILING DATE: [illegible]-26
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: GB [illegible]
;  PRIOR FILING DATE: [illegible]-04
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: [illegible]-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: [illegible]
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; PREV APPLICATION NUMBER: PCT/US01/xxxx
; PREV FILING DATE: 2001-xx-xx
; PREV APPLICATION NUMBER: PCT/US01/xxxx
; PREV FILING DATE: 2001-xx-xx
; PREV APPLICATION NUMBER: PCT/US01/xxxx
; PREV FILING DATE: 2001-01-30
; PREV APPLICATION NUMBER: US 09/xxx,xxx
; PREV FILING DATE: 2000-09-21
; PREV APPLICATION NUMBER: US 09/xxx,xxx
; PREV FILING DATE: 2000-08-xx
; PREV APPLICATION NUMBER: US 09/xxx,xxx
; PREV FILING DATE: 2000-01-29
; NUMBER OF SEQ ID NOS: 5417
; SOFTWARE: AmineMax Sequence Listing Editor Vers. 1.0
; SEQ ID NO 5417
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAY BE ACYLATED
; OTHER INFORMATION: EXPRESSED IN CLONE SENA
; OTHER INFORMATION: SWISSPROT HITS P10275, EVALUE 2.9e-7
; OTHER INFORMATION: BLT HUMAN 0111, 2001, Score 1742
US-09-864-761-5417

Query Match 2.1%; Score 82; DB 10; Length xxxx;
Best Local Similarity 100.0%; Pred. No. x.1;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTWCAIGDEC 10
| | | | | | | | | | |
Db 1 TCTWCAIGDEC 10

RESULT 4
US-09-864-761-5418
; Sequence 5418, Application US/09864761
; Patent No. US20020177155A1
; GENERAL INFORMATION:
; APPLICANT: TEEMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF CELIAC DISEASE
; FILE REFERENCE: 9475PA
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,128
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 5466
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 5418
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-761-5418

Query Match 2.1%; Score 82; DB 10; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTSHEEIEV 10
| | | | | | | | | | |
Db 1 TCTSHEEIEV 10

RESULT 5
US-09-864-761-5419
; Sequence 5419, Application US/09864761
; Patent No. US20020177155A1
; GENERAL INFORMATION:
; APPLICANT: Boston Biomedical, Inc.
; TITLE OF INVENTION: STAT PROTEIN VI AND SEQ ID NO:
; FILE REFERENCE: 7854.244
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23

; PREV APPLICATION NUMBER: 09/xxx,xxx
; PREV FILING DATE: 2000-05-30
; PREV APPLICATION NUMBER: 60/xxx,xxx
; PREV FILING DATE: 2000-02-11
; PREV APPLICATION NUMBER: 09/454,824
; PREV FILING DATE: 1999-12-06
; PREV APPLICATION NUMBER: 09/xxx,xxx
; PREV FILING DATE: 1999-05-xx
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-864-761-12

Query Match 2.1%; Score 82; DB 10; Length 651;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPLWSAQPPP 10
| | | | | | | | | | |
Db 541 TPLWSAQPPP 550

RESULT 6
US-09-864-761-4
; Sequence 4, Application US/09864761
; Patent No. US20020004204A1
; GENERAL INFORMATION:
; APPLICANT: Hawkes, Tana M
; APPLICANT: George, H. Reuben
; TITLE OF INVENTION: Electrochemical Probes for Detection of Molecules
; TITLE OF INVENTION: Interactions and Distances
; FILE REFERENCE: 97062.B
; CURRENT APPLICATION NUMBER: US/09/019,622
; CURRENT FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 60/037,939
; EARLIER FILING DATE: 1997-02-06
; EARLIER APPLICATION NUMBER: 60/050,449
; EARLIER FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SBH
; OTHER INFORMATION: Duplex
US-09-019-622-4

Query Match 2.1%; Score 82; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e-04;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 967 RTTTTGC 973
| | | | | | |
Db 1 RTTTTGC 7

RESULT 7
US-09-864-761-45
; Sequence 45, Application US/09864761
; Patent No. US20020042455A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; PUTTMAN, Neil
; KAY, Brian K.
; HAWKES, Tana M.
; MACONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND-

; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fenwick & Edwards LLP
; STREET: 1177 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: [illegible]
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/873,417
; FILING DATE: 04-Jun-2001
; CLASSIFICATION: Unknown
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/[illegible]
; FILING DATE: 03-Apr-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 11113-173
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 700-7000
; TELEFAX: (212) 223-4783
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-873-417-4

Query Match 2.1%; Score 7; DB 2; Length 7
Best Local Similarity 100.0%; Pred. No. 8.6e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 [illegible] 7
[illegible]
Db 1 [illegible] 7

RESULT 28
US-09-873-417-11
; Sequence 11, Application US/09873417
; Patent No. US20020019041A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; SPARKS, ANDREW D.
; THORN, [illegible] M.
; [illegible]AM, LAWRENCE A.
; DEN, CHANNING J.
; TITLE OF INVENTION: SOLUBLE PEPTIDE LIBRARIES AND METHODS FOR
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ORLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 500
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/[illegible]
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: [illegible]
; ATTORNEY/AGENT INFORMATION:
; NAME: Vitaliano, Gisele M.
; REGISTRATION NUMBER: 43,808
; REFERENCE/DOCKET NUMBER: 4980-0127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248540 PTOA
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid

```
                  Type: DNA
          Molecule type: peptide
          Sequence with (s): SEQ ID NO: 13

  Query Match                 Score 7; DB 10; Length 14;
  Best Local Similarity   Pred. No.
  Matches    7; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Qy      1 PEPTIDE 7
          ||||||
Db      1 PEPTIDE 7


RESULT 10
; Sequence 7, Application US/09875057
; Patent No. US20030166841A1
; GENERAL INFORMATION:
;       APPLICANT: SPEARS, Andrew B.
;                  HOFFMAN, Nancy [US_only,09/875,057]
;                  KAY, Brian K.
;                  POWERS, Dana M.
;                  MacDONNELL, Stephen J.
;       TITLE OF INVENTION: POLYPEPTIDES HAVING A PENTAPEPTIDE
;                           DOMAIN OF INTEREST AND METHODS
;                           USING SAME
;       NUMBER OF SEQUENCES: 227
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Dewitt & Edmonds LLP
;            STREET: 1175 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC DOS/MS DOS
;            SOFTWARE: Patentin Release #1.0, Version #1.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/875,057
;            FILING DATE: 04-Jun-2001
;            CLASSIFICATION: Unknown
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/856,875
;            FILING DATE: 14-May-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Minnock, S. Leslie
;            REGISTRATION NUMBER: 38,872
;            REFERENCE/DOCKET NUMBER: 1101-171
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869 8864/9741
;            TELEX: 66141 DEWITT
;    INFORMATION FOR SEQ ID NO: 179:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 13 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: Unknown
;            TOPOLOGY: unknown
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 179:
US-09-875-057-179

  Query Match                 Score 7; DB 10; Length 13;
  Best Local Similarity   Pred. No.
  Matches    7; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Qy      1 PEPTIDE 7
          |||||||
Db      1 PEPTIDE 7


RESULT 11
; Sequence 7, Application US/09875057
; Patent No. US20030166841A1
; GENERAL INFORMATION:
;       APPLICANT: SPEARS, Andrew B.
;                  HOFFMAN, Nancy [US_only,09/875,057]
;                  KAY, Brian K.
;                  POWERS, Dana M.
;                  MacDONNELL, Stephen J.
;       TITLE OF INVENTION: POLYPEPTIDES HAVING A PENTAPEPTIDE
;                           DOMAIN OF INTEREST AND METHODS
;                           USING SAME
;       NUMBER OF SEQUENCES: 227
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Dewitt & Edmonds LLP
;            STREET: 1175 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC DOS/MS DOS
;            SOFTWARE: Patentin Release #1.0, Version #1.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/875,057
;            FILING DATE: 04-Jun-2001
;            CLASSIFICATION: Unknown
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/856,875
;            FILING DATE: 14-May-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Minnock, S. Leslie
;            REGISTRATION NUMBER: 38,872
;            REFERENCE/DOCKET NUMBER: 1101-171
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869 8864/9741
;            TELEX: 66141 DEWITT
;    INFORMATION FOR SEQ ID NO: 179:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 13 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: Unknown
;            TOPOLOGY: unknown
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 179:
US-09-875-057-179

  Query Match                 Score 7; DB 10; Length 13;
  Best Local Similarity   Pred. No.
  Matches    7; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Qy      1 PEPTIDE 7
          |||||||
Db      1 PEPTIDE 7


RESULT 12
; Sequence 65, Application US/09880142
; Patent No. US20020119149A1
; GENERAL INFORMATION:
;  APPLICANT: Kenton, John
;  APPLICANT: Roberts, Steven
;  TITLE OF INVENTION: PROTEIN KINASE PROTEIN LEVELS IN BIOLOGICAL SAMPLES
;  FILE REFERENCE: 2727.2
;  CURRENT APPLICATION NUMBER: US/09/880,142
;  CURRENT FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: 60/211,780
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/211,841
;  PRIOR FILING DATE: 2000-06-15
;  NUMBER OF SEQ ID NOS: 67
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Kinase Recognition Sequence
US-09-503-387-4

Query Match 2.1%; Score 7; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRRRRRR 14
|||||||
Db 8 RRRRRRR 14

RESULT 43
US-09-503-387-5
; Sequence 5, Application US/09503387
; Patent No. US20020147345A1
; GENERAL INFORMATION:
; APPLICANT: Kenten, John
; APPLICANT: Roberts, Steven
; TITLE OF INVENTION: ONE-STEP CLINICAL IMMUNOASSAY
; FILE REFERENCE: 2757.5
; CURRENT APPLICATION NUMBER: US/09/503,387
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/120,047
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/119,911
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Kinase Recognition Sequence
US-09-503-387-5

Query Match 2.1%; Score 7; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRRRRRR 14
|||||||
Db 8 RRRRRRR 14

RESULT 44
US-09-503-387-6
; Sequence 6, Application US/09503387
; Patent No. US20020147345A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, Nov. US20020147345A1
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: McCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A PROLINE-RICH DOMAIN OF INTEREST AND METHODS FOR USING THE SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennie & Edwards LLP
; STREET: 2165 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,387
; FILING DATE: 14-Feb-2000
; CLASSIFICATION: Unknown
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/119,911
; FILING DATE: 12-FEB-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrick, S. Leslie
; REGISTRATION NUMBER: 34,872
; REFERENCE/DOCKET NUMBER: 2757.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 812-8570
; TELEX: 66141 DENNIE
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 147:
US-09-503-387-147

Query Match 2.1%; Score 7; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRRRRRR 14
|||||||
Db 8 RRRRRRR 14

RESULT 45
US-09-503-387-7
; Sequence 7, Application US/09503387
; Patent No. US20020147345A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, Nov. US20020147345A1
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: McCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A PROLINE-RICH DOMAIN OF INTEREST AND METHODS FOR USING THE SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennie & Edwards LLP
; STREET: 2165 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,387
; FILING DATE: 14-Feb-2000
; CLASSIFICATION: Unknown
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/119,911
; FILING DATE: 12-FEB-1999
; ATTORNEY/AGENT INFORMATION:

Query Match 2.1%; Score 7; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRRRRRR 14
|||||||
Db 8 RRRRRRR 14

RESULT 46
US-09-503-387-8
; Sequence 8, Application US/09503387
; Patent No. US20020147345A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, Nov. US20020147345A1
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: McCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A PROLINE-RICH DOMAIN OF INTEREST AND METHODS FOR USING THE SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennie & Edwards LLP
; STREET: 2165 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,387
; FILING DATE: 14-Feb-2000
; CLASSIFICATION: Unknown
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/119,911
; FILING DATE: 12-FEB-1999
; ATTORNEY/AGENT INFORMATION:

```
                NAME: Mostofsky, S. Leslie
                REGISTRATION NUMBER: 36,872
                REFERENCE/DOCKET NUMBER: 21-1 124
          TELECOMMUNICATION INFORMATION:
                TELEPHONE: (212) 790-9090
                TELEFAX: (212) 869-8864/8741
                TELEX: 66141 PENNIE
    INFORMATION FOR SEQ ID NO: 1644:
          SEQUENCE CHARACTERISTICS:
                LENGTH: 14 amino acids
                TYPE: amino acid
                STRANDEDNESS: Unknown
                TOPOLOGY: Unknown
          MOLECULE TYPE: peptide
          SEQUENCE DESCRIPTION: SEQ ID NO: 1644:
US-09-503-387-3-1644

  Query Match                 2.1%;  Score 7;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GLTPEEP 7
          |||||||
Db      8 GLTPEEP 14


RESULT 15
US-09-503-387-3-1645
; Sequence 1645, Application US/09/503,387
; Patent No. US20020028457A1
; GENERAL INFORMATION:
;   APPLICANT: SEARLS, Andrew B.
;                    BERMAN, Neil Stanford
;                    KAY, Brian K.
;                    LOWLESS, David M.
;                    MCCONNELL, Stephen J.
;   TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
;                       DOMAIN OF INTEREST AND METHODS FOR IDENTIFYING AND
;                       USING SAME
;   NUMBER OF SEQUENCES: 227
;   CORRESPONDENCE ADDRESS:
;        ADDRESSEE: Fennie & Edmonds LLP
;        STREET: 1155 Avenue of the Americas
;        CITY: New York
;        STATE: New York
;        COUNTRY: USA
;        ZIP: 10036-2711
;   COMPUTER READABLE FORM:
;        MEDIUM TYPE: Floppy disk
;        COMPUTER: IBM PC Compatible
;        OPERATING SYSTEM: PC-DOS/MS-DOS
;        SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/09/503,387
;        FILING DATE: 14-Feb-2000
;        CLASSIFICATION: Unknown
;   PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: US-08/600,013
;        FILING DATE: 09-FEB-1996
;   ATTORNEY/AGENT INFORMATION:
;        NAME: Mostofsky, S. Leslie
;        REGISTRATION NUMBER: 36,872
;        REFERENCE/DOCKET NUMBER: 21-1 124
;   TELECOMMUNICATION INFORMATION:
;        TELEPHONE: (212) 790-9090
;        TELEFAX: (212) 869-8864/8741
;        TELEX: 66141 PENNIE
;    INFORMATION FOR SEQ ID NO: 1645:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 21 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: Unknown
;             TOPOLOGY: Unknown
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1645:
US-09-503-387-3-1645

  Query Match                 2.1%;  Score 7;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GLTPEEP 7
          |||||||
Db      8 GLTPEEP 14


RESULT 16
US-09-503-387-3-1646
; Sequence 1646, Application US/09/503,387
; Patent No. US20020028457A1
; GENERAL INFORMATION:
;   APPLICANT: Xu, Xiaozhen
;   APPLICANT: Dillon, Patricia
;   APPLICANT: Mitchum, Jennifer L.
;   APPLICANT: Barlocker, Susan L.
;   APPLICANT: Jiang, Yuqi
;   APPLICANT: Henderson, Robert A.
;   APPLICANT: Kallos, Michael S.
;   APPLICANT: Hooper, Gary R.
;   APPLICANT: Potter, Mark W.
;   APPLICANT: Stolk, John A.
;   APPLICANT: Day, Sraid R.
;   APPLICANT: Vedvick, Thomas S.
;   APPLICANT: Carter, Darrick
;   APPLICANT: Li, Simon
;   APPLICANT: Wang, Alina
;   APPLICANT: Skerky, Yasir A.W.
;   APPLICANT: Hopfer, William
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;   TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;   FILE REFERENCE: 21012/1427C23
;   CURRENT APPLICATION NUMBER: US/09/503,387
;   CURRENT FILING DATE: 2000-02-14
;   NUMBER OF SEQ ID NOS: 2034
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1646
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-503-387-3-1646

  Query Match                 2.1%;  Score 7;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GLTPEEP 7
          |||||||
Db      8 GLTPEEP 14


RESULT 17
US-09-503-387-3-1647
; Sequence 1647, Application US/09/503,387
; Patent No. US20020028457A1
; GENERAL INFORMATION:
;   APPLICANT: Xu, Xiaozhen
;   APPLICANT: Dillon, Patricia
;   APPLICANT: Mitchum, Jennifer L.
;   APPLICANT: Barlocker, Susan L.
;   APPLICANT: Jiang, Yuqi
;   APPLICANT: Henderson, Robert A.
;   APPLICANT: Kallos, Michael S.
;   APPLICANT: Hooper, Gary R.
;   APPLICANT: Potter, Mark W.
;   APPLICANT: Stolk, John A.
;   APPLICANT: Day, Sraid R.
```

; APPLICANT: Vodkin, Lucas S
; APPLICANT: Sutter, Patrick
; APPLICANT: Li, Sarah
; APPLICANT: Wang, Aiqiu
; APPLICANT: Shokey, Yasir A.W.
; APPLICANT: Hopper, William
; APPLICANT: Bilyeu, John
; APPLICANT: McNeil, Patricia D.
; APPLICANT: Beuselinck, Raymond J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS For [illegible]
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 913
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 558
; LENGTH: 71
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-558

Query Match [illegible]; Score 71; DB [illegible]; Length 71;
Best Local Similarity [illegible]; Pred. No. 2.2;
Matches 71; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]
[illegible]
Db [illegible]

RESULT 5
US-09-822-827-555
; Sequence 555, Application US/09822827
; Patent No. US20020086847A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS For [illegible]
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.5401C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 555
; LENGTH: 71
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-555

Query Match [illegible]; Score 71; DB [illegible]; Length 71;
Best Local Similarity [illegible]; Pred. No. 2.2;
Matches 71; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]
[illegible]
Db [illegible]

RESULT 6
US-09-780-669-559
; Sequence 559, Application US/09780669
; Patent No. US20020086847A1
; GENERAL INFORMATION:
; APPLICANT: Shokey, Yasir A.
; APPLICANT: McCosh, Donald Alan
; APPLICANT: Flint, Steven L.
; APPLICANT: Xu, Jianchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS For [illegible]
; TITLE OF INVENTION: AND DIAGNOSIS OF [illegible]
; FILE REFERENCE: 210121.4847C
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 913
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 559
; LENGTH: 71
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-559

Query Match [illegible]; Score 71; DB [illegible]; Length 71;
Best Local Similarity [illegible]; Pred. No. 2.2;
Matches 71; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]
[illegible]
Db [illegible]

RESULT 7
US-09-822-827-554
; Sequence 554, Application US/09822827
; Patent No. US20020086847A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianchun
; APPLICANT: Shokey, John A.
; APPLICANT: Aiqiu, Paul A.
; APPLICANT: Flint, Steven L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS For THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.4847C
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 554
; LENGTH: 71
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-554

Query Match [illegible]; Score 71; DB [illegible]; Length 71;
Best Local Similarity [illegible]; Pred. No. 2.2;
Matches 71; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]
[illegible]
Db [illegible]

Search completed: December 5, 2002, 07:04:0
Job time : 21 secs

OM protein - protein search, using sw model

Run on: December [illegible], 2002, [illegible] ; Search time [illegible]
(without alignments)
[illegible] Million cell updates/sec

Title: US-09-503-387-3
Perfect score: [illegible]
Sequence: 1 MS[illegible]SEIALF[illegible]GIEVPA[illegible]K[illegible]

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 23422322 residues

Total number of hits satisfying chosen parameters: [illegible]

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: [illegible]
4: /cgn2_6/ptodata/1/iaa/[illegible]COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/[illegible]:*
6: /cgn2_6/ptodata/1/iaa/[illegible]:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1786	100.0	339	4	US-09-345-468-3	Sequence 3, Appli
2	1786	100.0	339	4	US-09-414-[illegible]A-3	Sequence 3, Appli
3	1678	94.0	319	4	US-09-345-468-[illegible]	Sequence [illegible], Appli
4	1678	94.0	319	4	US-09-414-453A-5	Sequence [illegible], Appli
5	1304	73.0	249	4	US-09-345-[illegible]	Sequence [illegible], Appli
6	1304	73.0	249	4	US-09-414-453A-[illegible]	Sequence [illegible], Appli
7	1122	62.8	[illegible]	4	US-09-[illegible]	Sequence [illegible], Appli
8	1122	62.8	313	4	US-09-414-453A-16	Sequence 16, Appli
9	1080.5	60.5	292	4	US-09-345-46[illegible]	Sequence [illegible], Appli
10	1080.5	60.5	292	4	US-09-414-453A-18	Sequence 18, Appli
11	937	52.5	267	4	US-09-345-468-[illegible]	Sequence [illegible], Appli
12	937	52.5	267	4	US-09-414-453A-1[illegible]	Sequence 1[illegible], Appli
13	498	27.9	448	4	US-09-310-463-18	Sequence 18, Appli
14	498	27.9	448	4	US-08-842-248A-18	Sequence 18, Appli
15	477	26.7	289	4	US-09-[illegible]-12	Sequence [illegible], Appli
16	477	26.7	289	4	US-08-842-248A-12	Sequence 12, Appli
17	455	25.5	299	4	US-09-310-463-[illegible]	Sequence [illegible], Appli
18	454	25.4	631	4	US-09-345-468-12	Sequence 12, Appli
19	454	25.4	631	4	US-09-414-453A-1[illegible]	Sequence 1[illegible], Appli
20	449	25.1	631	4	US-09-310-463-2[illegible]	Sequence 2[illegible], Appli
21	449	25.1	631	4	US-08-842-[illegible]	Sequence [illegible], Appli
22	441	24.7	483	4	US-09-310-463-16	Sequence 16, Appli
23	441	24.7	483	4	US-08-842-248A-1[illegible]	Sequence [illegible], Appli
24	439.5	24.6	489	4	US-09-310-463-14	Sequence 14, Appli
25	439.5	24.6	489	4	US-08-842-248A-14	Sequence 14, Appli
26	438	24.5	431	4	US-08-985-950-14	Sequence 14, Appli
27	438	24.5	431	4	US-08-985-950-2[illegible]	Sequence 2[illegible], Appli
29	434	24.3	599	4	US-09-310-463-10	Sequence 10, Appli
29	434	24.3	599	4	US-08-842-248A-10	Sequence 10, Appli
30	434	24.3	615	4	US-08-985-950-16	Sequence 16, Appli
31	434	24.3	615	4	US-08-985-950-18	Sequence 18, Appli
32	429	24.0	596	4	US-09-310-463-22	Sequence 22, Appli
33	429	24.0	596	4	US-08-842-248A-22	Sequence 22, Appli
34	425.5	23.8	659	4	US-09-310-463-2	Sequence 2, Appli
35	425.5	23.8	659	4	US-08-842-248A-2	Sequence 2, Appli
36	425.5	23.8	659	4	US-08-985-950-22	Sequence 22, Appli
37	422	23.6	287	4	US-09-310-463-32	Sequence 32, Appli
38	421.5	23.6	652	4	US-09-310-463-4	Sequence 4, Appli
39	421.5	23.6	652	4	US-08-842-248A-4	Sequence 4, Appli
40	416.5	23.3	469	4	US-08-985-950-12	Sequence 12, Appli
41	408.5	22.9	439	4	US-09-310-463-8	Sequence 8, Appli
42	408.5	22.9	439	4	US-08-842-248A-8	Sequence 8, Appli
43	397	22.2	285	4	US-09-310-463-34	Sequence 34, Appli
44	392	21.9	287	1	US-07-971-092-2	Sequence 2, Appli
45	392	21.9	287	6	5198342-2	Patent No. 5198342

ALIGNMENTS

RESULT 1
US-09-345-468-3
; Sequence 3, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Bastfield, S.
; APPLICANT: Villeval, J.
; APPLICANT: Jandrot Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: [illegible] AND USES THEREOF
; FILE REFERENCE: 7353-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-[illegible]
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-3

Query Match 100.0%; Score 1786; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 6.8e-1[illegible];
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 [illegible] 180

Qy 181 [illegible] 240
Db 181 [illegible] 240

Qy 241 [illegible]
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Qy 301 [illegible] 339
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RESULT 2
US-09-414-454A-4
; Sequence 4, Application US/09414454A
; Patent No. 6984779
; GENERAL INFORMATION:
; APPLICANT: Bustin-Ed, S.
; APPLICANT: Villevat, J.
; APPLICANT: Jandrot Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7851-147
; CURRENT APPLICATION NUMBER: US/09/414,454A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,498
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-454A-4

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Best Local Similarity 100.0%; Pred. No. 7.6e-140;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-414-454A-5
; Sequence 5, Application US/09414454A
; Patent No. 6984779
; GENERAL INFORMATION:
; APPLICANT: Bustin-Ed, S.
; APPLICANT: Villevat, J.
; APPLICANT: Jandrot Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7851-147
; CURRENT APPLICATION NUMBER: US/09/414,454A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,498
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-454A-5

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Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-414-454A-6
; Sequence 6, Application US/09414454A
; Patent No. 6984779
; GENERAL INFORMATION:
; APPLICANT: Bustin-Ed, S.
; APPLICANT: Villevat, J.
; APPLICANT: Jandrot Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7851-147
; CURRENT APPLICATION NUMBER: US/09/414,454A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,498
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-454A-6

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